

From: Prasad, Sarada
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Please perform a sequence search for the seq id no. 2 of this application.
This is an overdue amendment I acquired. I appreciate if this can be a rush.
thank you,

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Patent Examiner
Art Unit 1646
Room CM1-8B17
Tel: 703-305-1009

KM calcium-binding protein; calcium homeostasis; cardiac muscle;
 KM pumping capacity; myocardial cell; systolic calcium ion release;
 KM sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
 KM valve defect.
 OS Homo sapiens.
 XX DE19915485-A1.
 XX 19-OCT-2000.
 XX 07-APR-1999; 99DE-1015485.
 XX 07-APR-1999; 99DE-1015485.
 XX 07-APR-1999; 99DE-1015485.
 XX (KATU/) KATUS H A.
 XX (REMP/) REMPPIS A.
 XX Katus HA, Remppis A;
 XY WPI: 2000-673510/66.
 N-PSDB: C81814.
 XX Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency
 XX
 PS Claim 35; Page 22; 36pp; German.
 XX This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease.
 XX
 XX Sequence 95 AA;
 Query Match 41.5%; Score 194; DB 21; Length 95;
 Best Local Similarity 45.1%; Pred. No. 1.7e-14;
 Matches 41; Conservative 17; Mismatches 33; Indels 0; Gaps 0;
 OY 1 MTKLEHLEGYINIFHOVSVRKGHPDTLSKGEKOLLTKRELANTIKNKDAVIDEIOG 60
 DB 1 mteletamgmildvfrsrgsgstqtlkgeikvimekelpgfigsqdkdavidkild 60
 OY 61 LDANODEQVDFQEFISLVAIALKAHYHTRK 91
 DB 61 ldangdaqydfefivfaaltsachkyfek 91
 RESULT 15
 B45345
 ID B45545 standard; Protein; 95 AA.
 XX
 AC B45545;
 XX
 DT 22-FEB-2001 (first entry)
 XX
 DE Human S100P protein.

XX S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
 KM calcium-binding protein; calcium homeostasis; cardiac muscle;
 KM pumping capacity; myocardial cell; systolic calcium ion release;
 KM sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
 KM valve defect.
 OS Homo sapiens.
 XX DE19915485-A1.
 XX 19-OCT-2000.
 XX 07-APR-1999; 99DE-1015485.
 XX 07-APR-1999; 99DE-1015485.
 XX 07-APR-1999; 99DE-1015485.
 XX (KATU/) KATUS H A.
 XX (REMP/) REMPPIS A.
 XX Katus HA, Remppis A;
 XY WPI: 2000-673510/66.
 N-PSDB: C81815.
 XX Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency
 XX
 PS Claim 35; Page 23; 36pp; German.
 XX This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease.
 XX
 XX Sequence 95 AA;
 Query Match 41.5%; Score 194; DB 21; Length 95;
 Best Local Similarity 45.1%; Pred. No. 1.7e-14;
 Matches 41; Conservative 17; Mismatches 33; Indels 0; Gaps 0;
 OY 1 MTKLEHLEGYINIFHOVSVRKGHPDTLSKGEKOLLTKRELANTIKNKDAVIDEIOG 60
 DB 1 mteletamgmildvfrsrgsgstqtlkgeikvimekelpgfigsqdkdavidkild 60
 OY 61 LDANODEQVDFQEFISLVAIALKAHYHTRK 91
 DB 61 ldangdaqydfefivfaaltsachkyfek 91

Search completed: June 8, 2001, 15:03:24
 Job time: 24 sec

KW calcium-binding protein; calcium homeostasis; cardiac muscle;
 KW pumping capacity; myocardial cell; systolic calcium ion release;
 KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
 KW valve defect.
 OS Homo sapiens.
 PI DE19915485-A1.
 XX
 XX 19-OCT-2000.
 PD
 XX
 XX 07-APR-1999; 99DE-1015485.
 PE
 XX
 XX 07-APR-1999; 99DE-1015485.
 PR
 XX
 XX (KATV/) KATVS H A.
 PA (REMP/) REMPPIS A.
 XX
 XX Katus HA, Remppis A;
 PI

WPI: 2000-673510/66.
 N-PSDB; C81809.

Composition containing S100 protein, corresponding nucleic acid or vector, useful for treating cardiomyopathy and cardiac insufficiency.

PS Claim 35, Page 16-17; 36pp; German.
 XX
 XX This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease.

Sequence 114 AA:

Query Match 45.8%; Score 214.5; DB 21; Length 114;
 Best Local Similarity 46.7%; Pred. No. 1,1e-16;
 Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;
 QY 1 MTKLEHLEGIIVIFHOYSVRKGFDTLSKGLKQLTRELANTI-KNIKRAVIDEIRQ 59
 DB 5 mesqlenietlntfngysvkilghpdtlmgelkeivrkdlqflkknknevlehm 64
 QY 60 GLDANODEQVDQEFISLVAIALKAHNYHTK 91
 DB 65 dldtnadkqisfeefimmarltwashekme 96

RESULT 13
 Y87637
 ID Y87637 standard; Protein; 114 AA.
 AC
 XX Y87637;
 DT 04-AUG-2000 (first entry)
 XX
 DE Human calcium-binding protein #2.

XX
 XX Calcium-binding protein; granule release; calgranulin; human;
 KW vascular membrane growth; adult respiratory distress syndrome;
 KW acute myocardial infarction; ischemic reperfusion disorder;
 KW glomerulonephritis; rheumatoid arthritis; chronic bronchitis;
 KW cerebral vascular disorder; asthma; peripheral circulation disturbance;
 KW angina pectoris; hypertension; multiple sclerosis.
 OS Homo sapiens.
 PI WO200018970-A1.
 XX
 XX 06-APR-2000.
 PD
 XX
 XX 28-SEP-1999; 99WO-JP05302.
 PE
 XX
 XX 29-SEP-1998; 98JP-0274574.
 PR
 XX
 XX (ASAH) ASAH KASEI KOGYO KK.
 PA
 XX
 XX Seto M, Fukuda K;
 PI

WPI: 2000-293189/25.
 N-PSDB; A11970.

Controlling the release of granules from cell system using activated calgranulin for screening substances for granule activating or inhibiting activity.

PS Disclosure; Page 39-40; 42pp; Japanese.
 XX
 XX This invention describes a novel method for controlling the release of
 CC granules by treating a cell system to increase or decrease activated
 CC calgranulin to enhance or depress the release of granules. Calgranulin
 CC is a calcium binding protein and can be used for controlling the release
 CC of granules from a cell system e.g. those involved with the inhibition of
 CC vascular membrane growth. Vascular membrane growth is associated with
 CC e.g. adult respiratory distress syndrome, acute myocardial infarction due
 CC to ischemic reperfusion disorders, glomerulonephritis, rheumatoid
 CC arthritis, chronic bronchitis, cerebral vascular disorders, asthma,
 CC peripheral circulation disturbance, angina pectoris, hypertension and
 CC multiple sclerosis. The new method is used for screening substances for
 CC their ability to activate or inhibit the release of granules. This
 CC sequence represents a human calcium-binding protein which is described in
 CC the method of the invention.

Sequence 114 AA:

Query Match 45.8%; Score 214.5; DB 21; Length 114;
 Best Local Similarity 46.7%; Pred. No. 1,1e-16;
 Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;
 QY 1 MTKLEHLEGIIVIFHOYSVRKGFDTLSKGLKQLTRELANTI-KNIKRAVIDEIRQ 59
 DB 5 mesqlenietlntfngysvkilghpdtlmgelkeivrkdlqflkknknevlehm 64
 QY 60 GLDANODEQVDQEFISLVAIALKAHNYHTK 91
 DB 65 dldtnadkqisfeefimmarltwashekme 96

RESULT 14
 B45544
 ID B45544 standard; Protein; 95 AA.
 AC
 XX B45544;
 DT 22-FEB-2001 (first entry)
 XX
 DE Human S100B protein.
 XX
 KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;

DB 65 dldtnadkqjsfeefimarlwashekme 96

RESULT 10

ID W60178 standard; Protein; 114 AA.

AC W60178;

DT 03-SEP-1998 (first entry)

DE Human calprotectin subunit MRP-14 protein.

KW Human; MRP-8; MRP-14; calprotectin; mineral precipitate; struvite;

KW calcium phosphate; kidney stone; renal calculi; struvite stone;

KW urinary tract infection.

OS Homo sapiens.

PN US5776348-A.

PF 07-FEB-1998.

PR 07-FEB-1995; 95US-0385241.

PA (MAST) MASSACHUSETTS INST TECHNOLOGY.

PI Asakura H, Dretler SP, Orme-Johnson WH, Selengut JD;

DR WPI; 1998-397914/34.

DR N-PSDB; V34698.

PT Inhibiting kidney stone formation - uses the protein calprotectin

PS Example 1; Columns 21-22; 19pp; English.

CC This represents a human calprotectin subunit MRP-14. This is used in
CC a method for inhibiting the formation of a mineral precipitate in a
CC solution which comprises providing a solution comprising component ions
CC of the mineral precipitate or its precursors and contacting the solution
CC with an effective amount of isolated calprotectin, or a derivative of it.
CC The method is useful for the inhibition of kidney stone formation (renal
CC calculi). Kidney stones are concentrations of inorganic and organic salts
CC that develop through crystal nucleation, aggregation and growth in the
CC kidneys, which then can block the ureter and if not passed to the
CC bladder, grow and become symptomatic. Struvite stones (MgNH4PO4) are
CC commonly found after urinary tract infection. The mechanisms of this and
CC other stone formation is unclear, but some urine compositions are known
CC to inhibit formation. One of the major components of these is a protein
CC factor calprotectin, which inhibits mineral precipitation. Calprotectin
CC can also be used to raise antibodies, which in turn can be used to detect
CC the protein in samples. The levels of calprotectin found in samples can
CC be compared to levels found in normal humans, and thus assuming increased
CC calprotectin correlates to indication of kidney stone formation, this
CC procedure can be used as a diagnostic tool.

XX Sequence 114 AA;

Query Match 45.8%; Score 214.5; DB 19; Length 114;

Best Local Similarity 46.7%; Pred. No. 1.1e-16; Indels 1; Gaps 1;

Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

OY 1 MTKLEHLEGIVIPHOYSVRKGFDTLSKGLKQLTKRELNTI-KNIKRAVIDEIRFO 59

DB 5 msqlemnietlntfhgsvkqhpdtlmgsetkvlrvdkqnfikknknekvlehme 64

OY 60 GIDANODEQVDFEFTISLVATLKAANYHTHK 91

DB 65 dldtnadkqjsfeefimarlwashekme 96

RESULT 11

ID Y48615 standard; Protein; 114 AA.

AC Y48615;

DT 08-DEC-1999 (first entry)

DE Human breast tumour-associated protein 76.

KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;

KW treatment; tumour; cytostatic; medication.

OS Homo sapiens.

PN DE19813839-A1.

PD 23-SEP-1999.

PF 20-MAR-1998; 98DE-1013839.

PR 20-MAR-1998; 98DE-1013839.

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Specht T, Hinzmann B, Schmitt A, Pflarsky C, Dahl E, Rosenthal A;

DR WPI; 1999-528981/45.

DR N-PSDB; 233673.

PT Human nucleic acid sequences and protein products from tumor breast

PS tissue, useful for breast cancer therapy -

PS Claim 25; 176; 188pp; German.

CC This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC activity against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer. Y48540-Y48617 represent protein fragments
CC encoded by the expressed sequence tags described in the method of the
CC invention.

XX Sequence 114 AA;

Query Match 45.8%; Score 214.5; DB 20; Length 114;

Best Local Similarity 46.7%; Pred. No. 1.1e-16; Indels 1; Gaps 1;

Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

OY 1 MTKLEHLEGIVIPHOYSVRKGFDTLSKGLKQLTKRELNTI-KNIKRAVIDEIRFO 59

DB 5 msqlemnietlntfhgsvkqhpdtlmgsetkvlrvdkqnfikknknekvlehme 64

OY 60 GIDANODEQVDFEFTISLVATLKAANYHTHK 91

DB 65 dldtnadkqjsfeefimarlwashekme 96

RESULT 12

ID B45539 standard; Protein; 114 AA.

AC B45539;

DT 22-FEB-2001 (first entry).

DE Human S100A9 protein.

KW S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;

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OY      2  TKLEHLEGIYINIFHOYSVRKGFHDTLSKGLKQLTKRELANTIKNIKDKAVIDEITQGL 61
      1  tkledhleglilnifhgysvrvghfdtlkrelkqllckelpkrlqntckdqpctldkltfcdl 60
Db      62  DANODEQVDFQEFISLVAILKAHAHYTHK 91
      61  dadkdavgsfeefvlysvrlkthldhkh 90

RESULT  8
ID      Y90765 standard; Protein; 90 AA.
XX
AC      Y90765;
XX
DE      18-AUG-2000 (first entry)
XX
DE      Bovine CAAFI acid sequence SEQ ID NO:4.
XX
KW      Bovine; EN-RAGE; extracellular novel RAGE binding protein;
KW      receptor for advanced glycation endproduct; inflammation; inhibition;
KW      antiinflammatory; immunoglobulin; cell surface molecule; septic shock;
KW      systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
KW      autoimmune disorder; inflammatory disorder.
XX
OS      Bos taurus.
XX
PN      WC0200020621-A1.
XX
PD      13-APR-2000.
XX
PF      06-OCT-1999; 99WO-0523303.
XX
PR      06-OCT-1998; 98US-0167705.
XX
PR      05-MAR-1999; 99US-0263312.
XX
PA      (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI      Schmidt AM, Stern D;
XX
DR      WPI; 2000-303794/26.
XX
PT      New human EN-RAGE (extracellular novel receptor for advanced glycation
PT      end products) peptide, useful for identifying anti-inflammatory
PT      compounds that inhibit its interaction with RAGE -
XX
Claim 2; Page 41; 132pp; English.

The present invention describes an isolated human EN-RAGE (extracellular
novel receptor for advanced glycation end products) peptide (PI). The
EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin
superfamily of cell-surface molecules. A compound capable of inhibiting
the interaction of EN-RAGE with RAGE is useful for the suppression of
inflammation resulting from systemic lupus erythematosus, inflammatory
lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
inflammatory disorder in which the recruitment of EN-RAGE containing
inflammatory cells occurs. The compound is also useful for the treatment
of systemic lupus erythematosus, inflammatory lupus nephritis in a
subject. The human EN-RAGE peptide is useful for identifying compounds
that inhibit its interaction with RAGE. The present sequence represents
the bovine CAAFI which shows homology to the human EN-RAGE N-terminal
amino acid sequence.
XX
SQ      Sequence 90 AA;

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Db      1  tkledhleglilnifhgysvrvghfdtlkrelkqllckelpkrlqntckdqpctldkltfcdl 60
OY      62  DANODEQVDFQEFISLVAILKAHAHYTHK 91
      61  dadkdavgsfeefvlysvrlkthldhkh 90
Db      61  dadkdavgsfeefvlysvrlkthldhkh 90

RESULT  9
ID      W17062 standard; Protein; 114 AA.
XX
AC      W17062;
XX
DE      16-JUL-1997 (first entry)
XX
DE      Human multidrug resistance protein 14 (MRP14).
XX
KW      Genetic engineering; MRP; multidrug resistance protein; transgenic;
KW      animal model; cell death inhibition; apoptosis; cell proliferation;
KW      HIV; human immunodeficiency virus; cancer; cystic fibrosis; neoplasia;
KW      tumour.
XX
OS      Homo sapiens.
XX
PN      U55614397-A.
XX
PD      25-MAR-1997.
XX
PF      22-FEB-1994; 94US-0200016.
XX
PR      22-FEB-1994; 94US-0200016.
XX
PA      (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI      Lagasse E, Weissman I;
XX
DR      WPI; 1997-224943/20.
XX
DR      N-PSDB; T68322.
XX
PT      Increasing life-span of mammalian haemato-lymphoid cells by
PT      transforming stem cells - with construct contg. cell-specific
PT      transcription initiator and gene encoding protein that increases
PT      lifetime, useful for drug screening and treatment
XX
PS      Example 1; Column 33-34; 34pp; English.
XX
CC      W17062 is the human MRP14 protein. The transcriptional initiator of the
CC      MRP8 gene was used in a construct for expressing an open reading frame
CC      that increase the lifespan of a mammalian haematolymphoid cell, e.g. the
CC      mammalian Bcl-2 gene, a CTR (cystic fibrosis transmembrane regulator)
CC      gene, the herpes virus thymidine kinase gene or an oncogene.
CC      Haematolymphoid cells are especially neutrophils and the construct
CC      doubles the lifespan of transgenic cells. Transgenic cells or
CC      transgenic animals produced are used for screening for substances and
CC      treatments that prevent or promote cell death. They can also be returned
CC      to the patient to modulate apoptosis, i.e. in the treatment of disorders
CC      related to abnormal cell proliferation or death. Typical applications
CC      are treatment of viral diseases, including HIV; cancer and cystic
CC      fibrosis.
XX
SQ      Sequence 114 AA;

Query Match 45.8%; Score 214.5; DB 18; Length 114;
Best Local Similarity 46.7%; Pred. No. 1.1e-16;
Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

OY      1  MTKLEHLEGIYINIFHOYSVRKGFHDTLSKGLKQLTKRELANTIKNIKDKAVIDEITQGL 59
      5  msqierlelelilnifhgysvrlkthldhkh 64
Db      60  GLDANODEQVDFQEFISLVAILKAHAHYTHK 91
      61  dadkdavgsfeefvlysvrlkthldhkh 90

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SQ Sequence 91 AA;

Query Match

Best Local Similarity 70.3%; Score 337; DB 20; Length 91;
 Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 2 TRKEEHLEGIIVNTHQSVRKGFHDTLSKGLKOLLTKRELANTIKNKRAVIDEIQGL 61
 Db 1 ttlehdleglntfhgsvrrlghydtlklrelkqltkelpnltnktdqgtcklfnql 60

OY 62 DANODEQVDFQEFISLVAIALKAHHTHKE 92
 Db 61 dangdeqvsfkefvvlvtdvltahdnhke 91

RESULT 6

W03563 standard; Protein; 92 AA.

W03563;

01-MAY-1997 (first entry)

Calcium binding protein CAAFL.

Calcium binding protein; bovine; amniotic epithelial cell; neutrophil;
 intracellular signal transduction; squamous epithelial cell; cancer;
 macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix;
 squamous cell carcinoma; skin; oesophagus; CAAFL; lung; blood disease.

Bos taurus.

EP731166-A2.

11-SEP-1996.

04-DEC-1995; 95EP-0119045.

06-MAR-1995; 95JP-0070468.

06-MAR-1995; 95JP-0045564.

(HITOMI) HITOMI J.

(TOFU) TONEN CORP.

HITOMI J, Kimura T, Yamaguchi K, Yamamura T;

WPI; 1996-403989/41.

N-PSDB; T39345.

New human or bovine calcium binding protein and related nucleic acid
 - is a marker for inflammation, neoplasia, skin and blood diseases

Claim 1; Page 21; 36pp; English.

This sequence represents the CAAFL calcium-binding protein isolated from
 bovine amniotic fluid. CAAFL belongs to the S100 protein family, which
 includes calyculin, MRP8, and MRP14. Intracellular calcium ion
 concentration is one of the key factors for intracellular signal
 transduction. The calcium signals are transduced by various
 calcium-binding proteins, such as the protein encoded by this sequence.
 CAAFL is normally expressed in squamous epithelial cells, neutrophils and
 macrophages, but atypical epithelial cells are negative for CAAFL and
 overexpression is observed in several types of cancer cells and
 neutrophils/macrophages infiltrating cancerous lesions. Detection of
 CAAFL (using antibodies in usual immunoassays) can be used to diagnose
 (or monitor) inflammation, neoplasia (particularly squamous cell
 carcinoma of the skin, oesophagus, lung and cervix), and skin and blood
 diseases.

Sequence 92 AA;

Query Match 68.2%; Score 319; DB 17; Length 92;
 Best Local Similarity 66.3%; Pred. No. 1.8e-28;
 Matches 61; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

OY 1 MKRLEHLEGIIVNTHQSVRKGFHDTLSKGLKOLLTKRELANTIKNKRAVIDEIQGL 60
 Db 1 mklehdleglntfhgsvrrlghydtlklrelkqltkelpnltnktdqgtcklfnql 60

OY 61 DANODEQVDFQEFISLVAIALKAHHTHKE 92
 Db 61 dangdeqvsfkefvvlvtdvltahdnhke 92

RESULT 7

W0764 standard; Protein; 90 AA.

W0764;

18-AUG-2000 (first entry)

Bovine corneal antigen (B-COA) acid sequence SEQ ID NO:3.

Bovine; EN-RAGE; extracellular novel RAGE binding protein;
 receptor for advanced glycation endproduct; inflammation; inhibition;
 anti-inflammatory; immunoglobulin; cell surface molecule; septic shock;
 systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia;
 autoimmune disorder; inflammatory disorder.

Bos taurus.

WO200020621-A1.

13-APR-2000.

06-OCT-1999; 99WO-US23303.

06-OCT-1998; 98US-0167705.

05-MAR-1999; 99US-0263312.

(UNCO) UNIV COLUMBIA NEW YORK.

Schmidt AM, Stern D;

WPI; 2000-303794/26.

New human EN-RAGE (extracellular novel receptor for advanced glycation
 end products) peptide, useful for identifying anti-inflammatory
 compounds that inhibit its interaction with RAGE -

Claim 2; Page 41; 132pp; English.

The present invention describes an isolated human EN-RAGE (extracellular
 novel receptor for advanced glycation end products) peptide (PI). The
 EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin
 superfamily of cell-surface molecules. A compound capable of inhibiting
 the interaction of EN-RAGE with RAGE is useful for the suppression of
 inflammation resulting from systemic lupus erythematosus, inflammatory
 lupus nephritis, septic shock, endotoxaemia, or an autoimmune or
 inflammatory disorder in which the recruitment of EN-RAGE containing
 inflammatory cells occurs. The compound is also useful for the treatment
 of systemic lupus erythematosus, inflammatory lupus nephritis in a
 subject. The human EN-RAGE peptide is useful for identifying compounds
 that inhibit its interaction with RAGE. The present sequence represents
 the bovine corneal antigen which shows homology to the human EN-RAGE
 N-terminal amino acid sequence.

Sequence 90 AA;

Query Match 66.0%; Score 309; DB 21; Length 90;

Best Local Similarity 65.6%; Pred. No. 2.3e-27;
 Matches 59; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcolemmal reticulum (SR) that causes cardiac
 CC disease.
 CC XX
 SQ Sequence 92 AA;

Query Match 100.0%; Score 468; DB 21; Length 92;
 Best Local Similarity 100.0%; Pred. No. 4,4e-45;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGFPLSKGLKQLTKRELANTIKIRKAVIDEIFQG 60
 DB 1 mtkleehlegiivnifhysvrkghfplskglkqltkrelantikirkavideifqg 60
 61 LDANODEVDFOEFLISVAIALKAHYHTKE 92
 DB 61 ldanodevdfgefislvaialkaahyhthke 92

RESULT 4
 W01826
 ID W01826 standard; Protein; 91 AA.
 AC W01826;
 DT 16-OCT-1997 (first entry)
 XX Component of bioactive metal RNA polypeptide.
 DE Bioactive; metal; RNA polypeptide; RNP; modulation; analysis;
 KW angiogenesis; vascular state; mammalian tissue; transfer; cell;
 KM genetic information; selective; alteration; nucleic acid content;
 KW leukocyte; pig; monocyto-CURNP.
 XX
 OS Sus scrofa.
 XX
 PN DE19628895-A1.
 PD 23-JAN-1997.
 PF 17-JUL-1996; 96DE-1028895.
 PE 18-AUG-1995; 95DE-1030500.
 XX 17-JUL-1995; 95DE-1025992.
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEMANDTEN.
 PI Hellmeyer IMG, Kieseletter S, Logemann E, Wissler JH;
 XX MPI: 1997-088586/09.
 DR N-PSDB; T62569.
 XX
 PT Bioactive metal RNA polypeptide - useful for modulating
 XX angiogenesis, etc.
 PS Claim 1; Page 15; 16pp; German.
 XX A novel bioactive metal RNA polypeptide (RNP) has a RNA component
 CC including the sequence 702568 and a polypeptide component having
 CC the sequence W01826, which is encoded by T62569. The RNP, or
 CC anti-RNP immunoglobulin, can be used to modulate and/or analyse
 CC angiogenesis and the vascular state of mammalian tissue, transfer
 CC genetic information in cells and selectively alter the nucleic
 CC acid content of cells.
 CC Leukocytes from pig's blood were cultured in medium, and the
 CC supernatant treated with NH4 sulphate at 35, 45 and 90% saturation
 CC to precipitate protein fractions. The residual supernatant was
 CC diluted to 45% NH4 sulphate saturation and concentrated by

CC ultrafiltration using a 0.5 kD membrane. The reenate was purified
 CC to give 8 mg of product described as monocyto-CURNP.
 CC XX
 SQ Sequence 91 AA;

Query Match 70.9%; Score 332; DB 18; Length 91;
 Best Local Similarity 70.3%; Pred. No. 6,4e-30;
 Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 2 TKLEHLEGIIVNIFHOYSVRKGFPLSKGLKQLTKRELANTIKIRKAVIDEIFQGL 61
 DB 1 tkleehlegiivnifhysvrkghfplskglkqltkrelantikirkavideifqgl 60
 OY 62 DANODEVDFOEFLISVAIALKAHYHTKE 92
 DB 61 danodevdfkervlvltadvltahnhke 91

RESULT 5
 W93819
 ID W93819 standard; peptide; 91 AA.
 AC W93819;
 DT 21-JUN-1999 (first entry)
 XX Angiotropin related protein derived peptide.
 DE Angiotropin related protein derived peptide.
 KW Angiotropin related protein; ARP; ternary complex; S100 protein;
 KW copper-containing ribonucleoprotein; copper; cell selective;
 KW morphogenic action; blood capillary endothelial cell; confluent;
 KW non-mitogenic induction; cell phenotype; three-dimensional organoid;
 KW spatiotemporal supracellular organisation; chemotropic; blood vessel;
 KW tissue neovascularisation; angiogenesis modulation.
 XX
 OS Synthetic.
 XX
 PN DE19811047-C1.
 PD 15-APR-1999.
 PF 13-MAR-1998; 98DE-1011047.
 PR 13-MAR-1998; 98DE-1011047.
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEMANDTEN.
 PI Brunner H, Kieseletter S, Koch-Pelster B, Kuhn E;
 XX MPI: 1999-216114/19.
 DR
 XX
 PT Copper-containing ribonucleoproteins - useful for modulating
 XX angiogenesis
 PS Disclosure; Page 2; 16pp; German.
 XX This invention describes novel copper-containing ribonucleoproteins
 CC which are ternary complexes of an S100 protein, copper ions, and
 CC RNA comprising the following consensus sequence or its complement
 CC GGAAAUUNNNUNUAAUGN1-6CUNNUNUUNNNNAANA0-1UAAACAUN0-5CUNNAGN0-
 CC 13AGAA-AUN0-16UUNACAG where N = G, A, U or C. The ribonucleoproteins are
 CC stated to have the following properties (1) cell-selective morphogenic
 CC action in vitro on isolated primary and/or cloned blood capillary
 CC endothelial cells in culture for the non-mitogenic induction of the
 CC change in cell phenotype from the confluent state, for non-mitogenic;
 CC alteration of the spatiotemporal supracellular organisation of cells;
 CC into three-dimensional organoid, capillary-like structures in culture;
 CC (2) a specific chemotropic action on blood vessels in vivo, (3) induction
 CC of directional growth of blood vessels in vivo and (4) induction of
 CC neovascularisation of tissues through directed ingrowth of blood vessels.
 CC Their use for modulating angiogenesis is claimed.

PT New human or bovine calcium binding protein and related nucleic acid
 PT - is a marker for inflammation, neoplasia, skin and blood diseases
 XX
 PS Claim 1; Page 24; 36pp; English.
 CC This sequence represents the CAAP1 calcium-binding protein isolated from
 CC human amniotic fluid. CAAP1 belongs to the S100 protein family, which
 CC includes calyculin, MRP8, and MRP14. Intracellular calcium ion
 CC concentration is one of the key factors for intracellular signal
 CC transduction. The calcium signals are transduced by various
 CC calcium-binding proteins, such as this protein. CAAP1 is normally
 CC expressed in squamous epithelial cells, neutrophils and macrophages, but
 CC atypical epithelial cells are negative for CAAP1 and overexpression is
 CC observed in several types of cancer cells and neutrophils/macrophages
 CC infiltrating cancerous lesions. Detection of CAAP1 (using antibodies in
 CC usual immunoassays) can be used to diagnose (or monitor) inflammation,
 CC neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
 CC lung and cervix), and skin and blood diseases.
 CC
 SQ Sequence 92 AA;
 Query Match 100.0%; Score 468; DB 17; Length 92;
 Best Local Similarity 100.0%; Pred. No. 4.4e-45;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKTLEHLEGIYNIHFQYSVRKGHPDTLSKGLKOLLTKELANTIKNKAVIDEIFQG 60
 DB 1 mtkleehlegiynihfgysvrkghtclskglkqlltkelantlknkxkavideifg 60
 OY 61 LDANODEQYDFOEFISLVAIALKAHRYTHKE 92
 DB 61 ldandeqydfgefislvalalkaahyhkhke 92
 RESULT 2
 ID W24137 standard; Protein: 92 AA.
 XX W24137;
 AC 28-JAN-1998 (first entry)
 DT Human chemotactic cytokine I.
 DE Human chemotactic cytokine I.
 XX Chemotactic cytokine; tumour; autoimmune disease; antagonist;
 KW agonist.
 XX Homo sapiens.
 MO9723640-A1.
 XX 03-JUL-1997.
 PD 26-DEC-1995; 95WO-US16871.
 PF 26-DEC-1995; 95WO-US16871.
 XX 26-DEC-1995; 95WO-US16871.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Alfonso P, Gentz R, Ni J, Su JY, Yu G;
 PI WPI: 1997-351075/32.
 DR N-PSDB; T85774.
 XX DNA encoding chemotactic cytokine I - used to treat, e.g. tumours,
 PT chronic infection, leukaemia, etc.
 XX
 PS Claim 12; Pages 48-49; 64pp; English.
 CC This is a human chemotactic cytokine I polypeptide. The encoding
 CC polynucleotide, along with a vector and a host cell can be used for the
 CC recombinant production of the chemotactic cytokine. Cytokine agonists

CC and antagonists can be used for the treatment of a patient requiring a
 CC chemotactic cytokine I and for the treatment of a patient requiring the
 CC inhibition of a chemotactic cytokine I polypeptide, respectively. The
 CC chemotactic cytokine is used to treat tumours, chronic infection,
 CC leukaemia and T-cell mediated autoimmune diseases.
 CC
 SQ Sequence 92 AA;
 Query Match 100.0%; Score 468; DB 18; Length 92;
 Best Local Similarity 100.0%; Pred. No. 4.4e-45;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MKTLEHLEGIYNIHFQYSVRKGHPDTLSKGLKOLLTKELANTIKNKAVIDEIFQG 60
 DB 1 mtkleehlegiynihfgysvrkghtclskglkqlltkelantlknkxkavideifg 60
 OY 61 LDANODEQYDFOEFISLVAIALKAHRYTHKE 92
 DB 61 ldandeqydfgefislvalalkaahyhkhke 92
 RESULT 3
 ID B45542 standard; Protein: 92 AA.
 XX B45542;
 AC 22-FEB-2001 (first entry)
 DT Human S100A12 protein.
 DE S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
 XX calcium-binding protein; calcium homeostasis; cardiac muscle;
 KW pumping capacity; myocardial cell; systolic calcium ion release;
 KW sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
 KW valve defect.
 XX Homo sapiens.
 OS DE19915485-A1.
 PN 19-OCT-2000.
 PD 07-APR-1999; 99DE-1015485.
 XX 07-APR-1999; 99DE-1015485.
 PF 07-APR-1999; 99DE-1015485.
 PR (KATU/) KATUS H A.
 XX (REMP/) REMPPIS A.
 PA Katus HA, Remppis A;
 PI WPI: 2000-673510/66.
 DR N-PSDB; C81812.
 XX Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency
 XX
 PS Claim 35; Page 20; 36pp; German.
 CC This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (I) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 8, 2001, 15:03:00 ; Search time 18.53 Seconds

(Without alignments)
283.811 Million cell updates/sec

Title: US-09-227-854-2

Sequence: 1 MTKLEHLEGIIVIFHOYSV.....EFLSLVALAKAHYHFKKE 92

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 390729 seqs, 57163235 residues

11 number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

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1: /SIDSE6/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSE6/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSE6/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSE6/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDSE6/gcgdata/geneseq/geneseq/AA1984.DAT:*
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7: /SIDSE6/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDSE6/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDSE6/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDSE6/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDSE6/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDSE6/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDSE6/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDSE6/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDSE6/gcgdata/geneseq/geneseq/AA1994.DAT:*
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19: /SIDSE6/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDSE6/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDSE6/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDSE6/gcgdata/geneseq/geneseq/AA2001.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	92	17	W03564
2	468	100.0	92	18	W21137
3	468	100.0	92	21	B45542
4	332	70.9	91	20	W01826
5	332	70.9	91	18	W38819
6	319	68.2	92	17	W03563
7	309	66.0	90	21	Y90765
8	309	66.0	90	21	Y90765
9	214.5	45.8	114	18	W17062
10	214.5	45.8	114	19	W60178
11	214.5	45.8	114	20	Y48615

Result No.	Score	Query Match	Length	DB ID	Description
12	214.5	45.8	114	21	B45539
13	214.5	45.8	114	21	Y87637
14	194	41.5	95	21	B45544
15	194	41.5	95	21	B45545
16	189	40.4	50	21	Y90763
17	182	38.9	91	19	W46607
18	170	36.3	74	21	G01409
19	161.5	34.5	94	21	B45531
20	158	33.8	93	18	W17061
21	158	33.8	93	19	W60177
22	158	33.8	93	21	B45538
23	157.5	33.7	101	13	Y87636
24	157.5	33.7	101	13	R20560
25	157.5	33.7	101	16	R80453
26	157.5	33.7	101	21	B37432
27	157.5	33.7	101	21	B45534
28	157	33.5	105	21	B45541
29	157	33.5	114	21	B58356
30	154	32.9	89	13	R23429
31	153.5	32.8	97	13	R26406
32	153.5	32.8	97	13	R27058
33	153.5	32.8	97	21	B45532
34	147.5	31.5	90	20	Y29553
35	147.5	31.5	90	21	B45536
36	147.5	31.5	90	21	B44476
37	146	31.2	110	21	B45535
38	142.5	30.4	90	21	Y37068
39	137.5	29.4	98	18	W27152
40	137.5	29.4	98	20	W82409
41	137.5	29.4	98	21	B45543
42	137.5	29.4	98	21	B07950
43	132	28.2	30	16	R85169
44	127.5	27.2	97	21	B45540
45	127.5	27.2	97	21	Y93605

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	468	100.0	92	17	W03564
2	468	100.0	92	18	W21137
3	468	100.0	92	21	B45542
4	332	70.9	91	20	W01826
5	332	70.9	91	18	W38819
6	319	68.2	92	17	W03563
7	309	66.0	90	21	Y90765
8	309	66.0	90	21	Y90765
9	214.5	45.8	114	18	W17062
10	214.5	45.8	114	19	W60178
11	214.5	45.8	114	20	Y48615

Fri Jun 8 15:09:52 2001

us-09-227-854-2.rpr

Page 7

	Query Match	Similarity	Score	DB 2:	Length	101:
Match	Local	43.8%	Pred. No. 4.2e-08;			
	35;	Conservative	19;	Mismatches	23;	Indels 3; Gaps 1;
OY	4	LEEHLEGIIVINIHQSVYKRGHEDTSLKSGELKQOLLKRELANTIKNIKDKRAVIDEIFQGLDA	63			
Db	5	LEELADIVYIVSTYHAKSGREGDKFKUNKTELKELTLRELPSFLGKRRIDEAFQKVMNSLDS	64			
OY	64	NODEQVDFQEE---FISLVAI	80			
Db	65	NRDNEVDQFEYCVFLSCIAM	84			

Search completed: June 8, 2001, 15:03:57
Job time: 52 sec

R.Presland, R.B.: Haydock, P.V.; Fleckman, P.; Nirunauksiri, W.; Dale, B.A.
 J. Biol. Chem. 267, 23772-23781, 1992
 A>Title: Characterization of the human epidermal profilaggrin gene. Genomic organization
 A:Reference number: A45135; MUID:93054736
 A:Accession: A45135
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-591 <PRE>
 A:Cross-references: GB:L01089; GB:M90967; NID:9190408; PIDN:AAA60177.1; PID:9553621
 A:Note: sequence extracted from NCBI backbone (NCBIRP:118773)
 C:Genetics:
 A:Gene: GDB:FIG
 A:Cross-references: GDB:119912; OMIM:135940
 A:Map position: 1q21-1q21
 C:Superfamily: unassigned calmodulin-related proteins; calmodulin repeat homology
 C:Keywords: EF hand; epidermis; polymorphism; tandem repeat
 F:49-81/Domain: calmodulin repeat homology <EF2>

Query Match 35.7%; Score 168; DB 2; Length 591;
 Best Local Similarity 39.1%; Pred. No. 1.1e-07;
 Matches 36; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

DB 1 MTKLEPHLEGIIVNFHQYSVRKGFHPTLSKGLKQLTKELANTIKNKAKAVIDEIFOG 60
 1 MTKLEPHLEGIIVNFHQYSVRKGFHPTLSKGLKQLTKELANTIKNKAKAVIDEIFOG 60
 DB 61 LDANODEQVDFOEFISLVATLAAHYHTRKE 92
 61 LDIDHNKKIDFEFLMVFLLAQAYESTRKE 92

RESULT 14

caigizazarin - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext_change 21-Jul-2000
 C:Accession: JQ1300; P00243; B41004
 R:Matanabe, M.; Ando, Y.; Todoroki, H.; Minami, H.; Hidaka, H.
 Biochem. Biophys. Res. Commun. 181, 644-649, 1991
 A>Title: Molecular cloning and sequencing of a cDNA clone encoding a new calcium binding
 A:Reference number: JQ1300; MUID:92095968
 A:Accession: JQ1300
 A:Molecule type: mRNA
 A:Residues: 1-102 <WAT>
 A:Cross-references: GB:D10586; GB:D90531; NID:9217745; PIDN:BA01443.1; PID:9217746
 A:Accession: P00243
 A:Molecule type: protein
 A:Residues: 25-49; 53-62 <WAT2>
 A:Experimental source: lung
 R:Todoroki, H.; Kobayashi, R.; Matanabe, M.; Minami, H.; Hidaka, H.
 J. Biol. Chem. 266, 18668-18673, 1991
 A>Title: Purification, characterization, and partial sequence analysis of a newly identified
 A:Reference number: A41004; MUID:92011625
 A:Accession: B41004
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 25-49; 53-58, 'Y', 60-62 <TOD>
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: calcium binding; EF hand
 F:9-43/Domain: calmodulin repeat homology <EF1>
 F:52-84/Domain: calmodulin repeat homology <EF2>

Query Match 35.7%; Score 167; DB 1; Length 102;

Best Local Similarity 40.0%; Pred. No. 2.1e-08;
 Matches 34; Conservative 16; Mismatches 35; Indels 0; Gaps 0;

DB 2 TKLEPHLEGIIVNFHQYSVRKGFHPTLSKGLKQLTKELANTIKNKAKAVIDEIFOG 61
 2 TKLEPHLEGIIVNFHQYSVRKGFHPTLSKGLKQLTKELANTIKNKAKAVIDEIFOG 61
 DB 5 TETERCESLIAVFOKAGDSVLTSTKTEFLSMTELAFTKOKDGVLDPMKKKL 64
 5 TETERCESLIAVFOKAGDSVLTSTKTEFLSMTELAFTKOKDGVLDPMKKKL 64
 QY 62 DANODEQVDFOEFISLVATLAAHYHTRKE 96
 62 DANODEQVDFOEFISLVATLAAHYHTRKE 96

DB 65 DLNSDGLDFQERFLNIGGLAVACH 89
 65 DLNSDGLDFQERFLNIGGLAVACH 89

RESULT 15

S06207

calvasculin - mouse

N:Alternate names: calcium-binding protein mtel; calcium-binding protein pEL98; pla
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #ext_change 20-Jun-2000
 C:Accession: S06207; JH0097; S07981; A26803; A4141; I46674
 R:Edraldize, A.; Tulchinsky, E.; Grigorian, M.; Afanasyeva, A.; Senin, V.; Revazova,
 Genes Dev. 3, 1086-1093, 1989
 A>Title: Isolation and characterization of a gene specifically expressed in differ

A:Reference number: S06207; MUID:89378739

A:Accession: S06207

A:Molecule type: mRNA

A:Residues: 1-101 <EBR>

A:Cross-references: EMBL:X16190; NID:954926; PIDN:CAA34316.1; PID:954927

R:Tulchinsky, E.M.; Grigorian, M.S.; Edraldize, A.K.; Mishina, N.I.; Lukanidin, E.

Gene 87, 219-223, 1990

A>Title: Structure of gene mtel, transcribed in metastatic mouse tumor cells.

A:Reference number: JH0097; MUID:90236313

A:Accession: JH0097

A:Molecule type: DNA

A:Residues: 1-101 <TUL>

A:Cross-references: GB:M36578; GB:M36579

A:Experimental source: liver

R:Tulchinsky, B.

A:Reference number: S07981

A:Accession: S07981

A:Molecule type: DNA

A:Residues: 1-47, 'VSGSXFGN', 56-57, 'RTDEAA', <TUL>

A:Cross-references: EMBL:X16094; NID:953249; PIDN:CAA344224.1; PID:953250

R:Jackson, G.; Swiergiel, J.; Linzer, D.I.H.

Nucleic Acids Res. 15, 6677-6690, 1987

A>Title: A growth-related mRNA in cultured mouse cells encodes a placental calcium

A:Reference number: A26803; MUID:87316927

A:Accession: A26803

A:Molecule type: mRNA

A:Residues: 1-101 <JAC>

A:Cross-references: GB:X05835; NID:950310; PIDN:CAA29282.1; PID:950311

R:Goto, K.; Endo, H.; Fujiyoshi, T.

J. Biochem. 103, 48-53, 1988

A>Title: Cloning of the sequences expressed abundantly in established cell lines: 1

A:Reference number: A41411; MUID:88198109

A:Accession: A41411

A:Molecule type: mRNA

A:Residues: 1-101 <GOT>

A:Cross-references: GB:D00208; NID:9220569; PIDN:BA00148.1; PID:9220570

R:Tulchinsky, E.; Kramerov, D.; Ford, H.L.; Reshetnyak, E.; Lukanidin, E.; Zain, S.

Oncogene 8, 79-86, 1993

A>Title: Characterization of a positive regulatory element in the mtel gene.

A:Reference number: I46674; MUID:93141279

A:Accession: I46674

A:Molecule type: DNA

A:Residues: 1-47, 'VSGSXFGN', 48-54 <RES>

A:Cross-references: EMBL:X16094; NID:953249; PIDN:CAA344224.1; PID:953250

C:Comment: Gene mtel is expressed in metastatic cells.

C:Genetics:

A:Gene: mtel

A:Introns: 47/3

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; cancer; EF hand

F:7-41/Domain: calmodulin repeat homology <EF1>

F:50-82/Domain: calmodulin repeat homology <EF2>

F:18,21,23,26,31/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
F:61,63,65,67,72/Binding site: calcium (Asp, Asp, Glu, Glu, Glu) #status predicted

Query Match

39.5%; Score 185; DB 1; Length 91;
Best Local Similarity 38.8%; Pred. No. 4,4e-10;
Matches 33; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

2 TKLEHLEGIYVNFHOYSVRKRGHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 61

1 SELEAAVALIDVFHOYSRGDKHKKLSKELINELSHLEEKDEVDKVMETL 60

62 DANODEQVDFEFLISVAIALKAAH 86

61 DSDGDGEDDFEFMAFAMITACH 85

RESULT 10

JN0686

calgranulin B - rat

Accession: JN0686; Species: Rattus norvegicus (Norway rat); Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 22-Jun-1999

R:Imamichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.

Biochem. Biophys. Res. Commun. 194, 819-825, 1993

A:Title: Expression and cloning of migration inhibitory factor-related protein (MRP) 8 an

A:Reference number: JN0685; MUID:93343942

A:Accession: JN0686

A:Molecule type: mRNA

A:Residues: 1-113 <IWA>

C:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; F

F:2-113/Product: calgranulin B #status predicted <MAT>

F:11-45/Domain: calmodulin repeat homology <EP1>

F:55-87/Domain: calmodulin repeat homology <EP2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:80-91/Disulfide bonds: #status predicted

F:80-91/Disulfide bonds: #status predicted

Query Match

38.6%; Score 180.5; DB 1; Length 113;

Best Local Similarity 38.5%; Pred. No. 1.4e-09;

Matches 35; Conservative 24; Mismatches 31; Indels 1; Gaps 1;

2 TKLEHLEGIYVNFHOYSVRKRGHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 60

7 SOLERSSTIINVFHOYSRKRGHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 60

61 LDANODEQVDFEFLISVAIALKAAH 91

67 LDTONQDQLSFECCMLMGLKLIFFACHEKHE 97

RESULT 11

S68242

calgranulin B - mouse

N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto

C:Species: Mus musculus (house mouse)

C:Date: 06-Sep-1996 #sequence_revision 23-May-1997 #text_change 22-Jun-1999

C:Accession: S68242; S68272

R:Tagase, E.; Weissman, I.L.

A:Description: Mouse MRP8 and MRP14, two intracellular calcium-binding proteins associat

A:Reference number: S68242

A:Accession: S68242

A:Molecule type: mRNA

A:Residues: 1-113 <LAG>

A:Cross-references: EMBL:M83219; NID:G199807; PIDN:AA07228.1; PID:G199808

R:Rafferty, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geezy, C.L.

Biochem. J. 316, 285-293, 1996
A:Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory-fa

ding.
A:Reference number: S68272; MUID:96235204

A:Accession: S68272

A:Molecule type: protein

A:Residues: 2-10;95-109 <RAF>

A:Note: 107-His is identified as 3'-methylhistidine; the authors' source for the re

ylhistidine

C:Gene: MRP14

C:Complex: heterodimer and higher complexes with calgranulin A

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflamma

F:2-113/Product: calgranulin B #status predicted <MAT>

F:11-45/Domain: calmodulin repeat homology <EP1>

F:55-87/Domain: calmodulin repeat homology <EP2>

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

F:80-91/Disulfide bonds: #status experimental

F:103-105/107/Binding site: zinc (His) #status predicted

F:107/Modified site: 3'-methylhistidine (His) #status experimental

Query Match

38.1%; Score 178.5; DB 1; Length 113;

Best Local Similarity 39.6%; Pred. No. 2.1e-09;

Matches 36; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

2 TKLEHLEGIYVNFHOYSVRKRGHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 60

7 SOMERSITTIIDVFHOYSRKRGHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 60

61 LDANODEQVDFEFLISVAIALKAAH 91

67 LDTONQDQLSFECCMLMGLKLIFFACHEKHE 97

RESULT 12

S35985

S-100 protein alpha chain - weatherfish

C:Species: Misgurnus fossilis (weatherfish)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S35985

R:Ivanenkov, V.V.; Gerke, V.; Minin, A.A.; Plessmann, U.; Weber, K.

Mech. Dev. 42, 151-158, 1993

A:Title: Transduction of Ca(2+) signals upon fertilization of eggs: identification

A:Reference number: S35985; MUID:94031845

A:Accession: S35985

A:Molecule type: protein

A:Residues: 1-95 <IWA>

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

F:49-81/Domain: calmodulin repeat homology <EP2>

Query Match

37.9%; Score 177.5; DB 1; Length 95;

Best Local Similarity 45.9%; Pred. No. 2.2e-09;

Matches 39; Conservative 16; Mismatches 29; Indels 1; Gaps 1;

2 TKLEHLEGIYVNFHOYSVRKRGHDTLSKGLKQLTKELANTIKNIKDKAVIDEIFOG 60

1 VSQLESAMESLIVFHYTSKRGDKYKLSKELKSLGELNDFLSKDPVYKIMSD 60

61 LDANODEQVDFEFLISVAIALKAA 85

61 LDENODEQVDFEFLVVA-ALNVA 84

RESULT 13

A45135

profilaggrin - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999

C:Accession: A45135

Biochim. Biophys. Acta 790, 164-173, 1984
 A:Title: Purification, characterization and ion binding properties of human brain S100b
 C:Reference number: A90653; PMID:85023393
 A:Contents: annotation; metal ion-binding properties
 C:Comment: This protein binds p53, tubulin and many other proteins at physiological concentrations
 C:Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tightly than different affinities exist for both ions on each monomer. Physiological concentrations of zinc are in the range of 10⁻¹⁰ M.
 C:Comment: This protein is expressed predominantly in brain tissue by astroglial cells.
 C:Comment: The homodimer contains disulfide bonds, but the bond pattern has not been determined.
 C:Gene: GDB:S100B
 A:Cross-references: GDB:120360; OMIM:176990
 A:Map position: 21q22.3-21q22.3
 A:Introns: 46/3
 A:Note: the first intron occurs before the initiator codon
 C:Complex: homodimer; heterodimer with S-100 protein alpha chain (see PIR:BCBU1A)
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; brain; calcium binding; EF hand; heterodimer; homodimer; S-100 protein; S-100 protein beta chain #status experimental <EPI>
 F:19-22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
 F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted
 F:92/Product: S-100 protein beta chain #status experimental <EPI>
 F:92/Domain: calmodulin repeat homology <EPI>
 F:98/Domain: calmodulin repeat homology <EPI>
 F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status experimental <EPI>
 F:19,22,24,27,32/Binding site: calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
 F:62,64,66,68,73/Binding site: calcium (Asp, Asp, Glu, Glu) #status predicted

Query Match 40.4%; Score 189; DB 1; Length 92;
 Best Local Similarity 39.5%; Pred. No. 2e-10;
 Matches 34; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

QY 1 MTKLEHLEGVNIFHGYSRKGFHDTLSKGLKLTRELATINIKKAVIDEIFOG 60
 DB 1 MSELKAMVALIDVFHGYSGEGDKHKLKSELKELINNELSHLEIKOEVDKVMET 60
 QY 61 LDANODEOVDFOEFTSLVAIALKAH 86
 DB 61 LDNDGEGCDFOEFMAFVAVTTACH 86

RESULT 8
 A26557
 S-100 protein beta chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 25-Mar-1988 #sequence, revision 04-Nov-1994 #text, change 13-Aug-1999
 C:Accession: A60046; S07357; A26557
 R:Maeda, T.; Usui, H.; Araki, K.; Kuwano, R.; Takahashi, Y.; Suzuki, Y.
 PNAS Res. Mol. Brain Res. 10, 193-202, 1991
 A:Title: Structure and expression of rat S-100 beta subunit gene.
 A:Reference number: A60046; PMID:91359841
 A:Accession: A60046
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-92 <MAE>
 A:Cross-references: GB:S53527
 R:Kuwano, R.; Usui, H.; Maeda, T.; Fukui, T.; Yamamori, N.; Ohtsuka, E.; Ikehara, M.; Tanabe, T.
 Nucleic Acids Res. 12, 7455-7465, 1984
 A:Title: Molecular cloning and the complete nucleotide sequence of cDNA to mRNA for S-100 beta subunit.
 A:Reference number: S07357; PMID:85037924
 A:Accession: S07357
 A:Molecule type: mRNA
 A:Residues: 1-92 <KUU>
 A:Cross-references: EMBL:X01090; NID:957174; PIDN:CA25567.1; PID:957175
 R:Dunn, R.; Landry, C.; O'Hanlon, D.; Dunn, J.; Allaire, R.; Brown, I.; Marks, A.
 J. Biol. Chem. 262, 3562-3566, 1987
 A:Title: Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells following treatment with retinoic acid.
 A:Reference number: A26557; PMID:87137648
 A:Accession: A26557
 A:Molecule type: mRNA
 A:Residues: 6-92 <DUN>
 A:Cross-references: GB:M15705
 C:Comment: S-100 protein occurs as alpha-beta heterodimers, alpha-alpha heterodimers, and

A:Introns: 46/3
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: brain; calcium binding; dimer; EF hand; zinc
 F:2-92/Product: S-100 protein beta chain #status predicted <MAT>
 F:6-40/Domain: calmodulin repeat homology <EPI>

Query Match 40.0%; Score 187; DB 2; Length 92;
 Best Local Similarity 38.4%; Pred. No. 3e-10;
 Matches 33; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 1 MTKLEHLEGVNIFHGYSRKGFHDTLSKGLKLTRELATINIKKAVIDEIFOG 60
 DB 1 MSELKAMVALIDVFHGYSGEGDKHKLKSELKELINNELSHLEIKOEVDKVMET 60
 QY 61 LDANODEOVDFOEFTSLVAIALKAH 86
 DB 61 LDNDGEGCDFOEFMAFVAVTTACH 86

RESULT 9
 BCOBIB
 S-100 protein beta chain - bovine
 N:Alternate names: neurocalcin delta-binding protein S100-beta
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-May-1979 #sequence, revision 14-Nov-1983 #text, change 24-Nov-1999
 R:Isobe, T.; Okuyama, T.
 Eur. J. Biochem. 89, 379-388, 1978
 A:Title: The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation to the S-100 protein family.
 A:Reference number: A91254; PMID:79045265
 A:Accession: A91254
 A:Molecule type: protein
 A:Residues: 1-91 <ISO>
 A:Experimental source: brain
 A:Note: this sequence has since been revised in reference A91110
 R:Isobe, T.; Okuyama, T.
 Eur. J. Biochem. 116, 79-86, 1981
 A:Title: The amino-acid sequence of the alpha subunit in bovine brain S-100 a protein.
 A:Reference number: A91110; PMID:81236562
 A:Accession: B91110
 A:Molecule type: protein
 A:Residues: 1-91 <ISO>
 R:Baudier, J.; Gerard, D.
 Biochemistry 22, 3360-3369, 1983
 A:Title: Ions binding to S100 proteins: structural changes induced by calcium and zinc.
 A:Reference number: A90471; PMID:84000339
 A:Contents: annotation; metal ion-binding properties
 R:Marshak, D.R.; Umekawa, H.; Watterson, D.M.; Hidaka, H.
 Arch. Biochem. Biophys. 240, 777-780, 1985
 A:Title: Structural characterization of the calcium binding protein S100 from adipose tissue.
 A:Reference number: A90075; PMID:85278169
 A:Accession: A90075
 A:Molecule type: protein
 A:Residues: 1-91 <MAE>
 A:Experimental source: adipose tissue
 R:Okazaki, K.; Obara, N.; Inoue, S.; Hidaka, H.
 Biochem. J. 306, 551-555, 1995
 A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in brain.
 A:Reference number: S54343; PMID:95194333
 A:Accession: S54348
 A:Molecule type: protein
 A:Residues: 56-61, 'N', 63-79, 'V' <OKA>
 C:Comment: The S-100 protein is composed of two related polypeptide chains, alpha and beta. The S-100 protein is also found in a variety of other tissues.
 C:Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc more tightly than different affinities exist for both ions on each monomer. Physiological concentrations of zinc are in the range of 10⁻¹⁰ M.
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; brain; calcium binding; EF hand; zinc
 F:5-39/Domain: calmodulin repeat homology <EPI>
 F:48-80/Domain: calmodulin repeat homology <EPI>
 F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental

A>Title: Molecular cloning, occurrence, and expression of a novel partially secreted protein
A:RefSeq accession number: A54327; MUID:92043866
A:Accession: D54327
A:Molecule type: protein
A:Residues: 11-19;26-38;94-105,'X',107 <MAD>
A:Note: In several peptide samples no PTH was detected for 95-His but in one peptide PTH
A:Comment: This protein appears to be expressed only in cells of myeloid origin actively
C:Comments: The presence of 3'-methylhistidine at position 105, corresponding to 107-His
C:Genetics:
A:Gene: GDB:SI100A3; 60B8AG; CAGB; CFAG; LIAG; MAC387; MIF; MRP14; NIF; P14
A:Cross-references: GDB:I20570; OMIM:I23886
A:Map position: 1q21-1q21
A:Introns: 50/3
A:Note: the first intron occurs before the initiator codon
C:Complex: heterodimer and higher complexes with calgranulin A (see PIR:BCHUCF)
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation; phospho
F:2-114/Product: calgranulin B #status experimental <MAT>
F:10-44/Domain: calmodulin repeat homology <EF1>
F:4-86/Domain: calmodulin repeat homology <EF2>
Modified site: blocked amino end (Thr) (in mature form) (probably acetylated) #status
...13/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match	45.8%	Score 214.5;	DB 1;	Length 114;
Best Local Similarity	46.7%	Pred. No. 1.3e-12;		
Matches 43; Conservative	22;	Mismatches 26;	Indels 1;	Gaps 1;

OY 60 GLDANODEQVDFEFTISVAIALKAHAYTHK 91
Db 65 DLDITNADKOLSEFEETIMLARLTAAHSHEMB 96

RESULT 5

S24146
S-100 protein P - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S24146; PS0340
R:Becker, T.; Gerke, V.; Kube, E.; Weber, K.
Eur. J. Biochem. 207, 541-547, 1992
A:Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA cloning, recombinant expression, and characterization of the protein.
A:Reference number: S24146; MUID:92339442
A:Accession: S24146
Status: preliminary

A:Residues: 1-95 <BCE>
A:Cross-references: EMBL:X65614; NID:q36177; PIDN:CA46566.1; PID:q36178
R:Emoto, Y.; Kobayashi, R.; Akatsuka, H.; Hidaa, H.
Biochem. Biophys. Res. Commun. 182, 1246-1253, 1992
A:Title: Purification and Characterisation of a new member of the S-100 protein family
A:Reference number: P50340; M0ID:9211935
A:Accession: P50340
A:Molecule type: Protein
A:Residues: 1-31, 'T', '33-84', 'X', '86-91 <EMO>
A:Experimental source: placenta
C:Genetics:
A:Gene: GDB:S100P
A:Cross-references: GDB:134405; OMIM:600614
A:Map position: 4p16-4p16
C:Superfamily: S-100 protein; calmodulin repeat homology
C:Keywords: calcium binding; EF hand; Placenta
F:6-40/Domain: calmodulin repeat homology <EFI>
F:49-81/Domain: calmodulin repeat homology <EF2>

Query Match	41.5%	Score 194;	DB 2;	Length 95;
Best Local Similarity	45.1%;	Pred. No. 7.3e-11;		
Matches	41;	Conservative	17;	Mismatches 33;
			Indels	0;
			Gaps	0

```
OY      1 MTKLEELSEIVINIFQVYSVRKNGHEPTLSKGSLKOLLREKLANITKNINKNOXKAVIDEFG 60
          |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      1 MTELETAMGNIIDVFERYSGSEGSPQTLLTGSGLAKLMEKELPGLSGSKRDADVKILD 60
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
OY      61 LDANQDQVDVDFEFISVALALKAAYHTHK 91
          |||||::||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 LDANGDAQVDSEFIVFAVAITSACKKKPKR 91
          |||||::||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

RESULT 6
A48015

S-100 protein beta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_rev1stlon 02-Jun-1995 #text_change 24-Nov-1995
C:Accession: A48015
R:Jiang, H.; Shah, S.; Hilt, D.C.
R:BioJ Chem 358 20502-20511 1992

J. Biol. Chem. 268, 20502-20511, 1993

A1: Title: Organization, sequence, and expression of the murine S100beta gene. TransA1: Reference number: A48015; M0ID:93388628

A;Accession: A48015
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-92 <JIA

A/Cross-References: GB:L22144; NID:g404768; PIDN:AAA03075.1; PID:g404769
C/Genetics:

A; Introns: 46/3

C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: acetylated amino end; calcium binding; EF hand

Accession	Product	Status	Predicted	Model
F5292	Product: S-100 protein beta chain	#status	Predicted	<MAT>
F5640	Product: S-100 protein beta chain	#status	Predicted	<MAT>

F:2/Modified site: acetylated amino end (Ser) (11)

F ₂₀	22	24	27	32	Binding site: calcium (Gly, Glu, Asp, Lys, Glu) #status predicted	
5.62	64	66	68	70	73	Binding site: calcium (Gly, Glu, Asp, Lys, Glu) #status predicted

```
.../01/00/00/01/0/dining site: calcium (asp, asp, glu, asp, glu) #status p
```

Query Match	40.68;	Score 190;	DB 2;	Length 92;
Best Local Similarity	39.58;	Pred. No. 1.6e-10;		
Matches 34;	Conservative 26;	Mismatches 26;	Indels 0;	Gaps 0

```

Qy 1 MRLKEHLEGIYVINFHVSXKRGHFDLTSKGLKOLLTRKLANIKINDKRAVIDEIPOG 60
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSLTEKAMVALIDVPHQYSGREGRKHKLKSEKSELKELINNELSHFEIEKEQVVDKVMET 60
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 LDANDQDQVDFQEFISIAIALKAAH 86
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LDQDGDGEGCDQEFMAFYAAVTYTTACH 86
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT

S-100 protein beta chain (validated) - human
BCHUIB
N:Alternate names: neural S-100 calcium-binding protein beta

C; Species: Homo sapiens (man)

C:\Date: 04-Dec-1986 #sequence_revision 06-Jan-1995 #text_change 08-Dec-2000
C:\Accession: A38364; A92972; A03076

R; Allore, R.J.; Friend, W.C.; O'Hanlon, D.; Nellson, K.M.; Baumann, R.; Dunn, R.J.; I B101 Chem 265 15537-15543 1990

A:Title: Cloning and expression of the human S100beta gene

A;Reference number: A38364; MUID:90368757

A: Accession: A38364

A;ResIdues: 1-92 <ALL>

A; Cross-references: GE

R; Jensen, R.; Marshak, D.R.; Anderson, C.; Lukas, T.J.; Watterson, D.M.
Neurochem 45: 700-705, 1985

A: Title: Characterization of human brain s100 protein fraction: amino acid composition

A;Reference number: A92972; MUID:85291729

A;Accession: A92972

A: Residue: 2-92 <TFN>

R; Baudler, J.; Glasser, N.; Haqild, K.; Gerard, D.

C:Keywords: calcium binding; EF hand; monomer; neutrophil; zinc
 F:2-92/Product: S-100 calcium-binding protein A12 #status experimental <MAT>
 F:6-39/Domain: calmodulin repeat homology <EF1>
 F:49-81/Domain: calmodulin repeat homology <EF2>
 F:66-90/Region: zinc binding #status predicted

Query Match 100.0%; Score 468; DB 2; Length 92;
 Best Local Similarity 100.0%; Pred. No. 26-35;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGHFDPLSKGELKOLLTELANTIKNKRAVIDEIFOG 60
 DB 1 MTKLEHLEGIIVNIFHOYSVRKGHFDPLSKGELKOLLTELANTIKNKRAVIDEIFOG 60

OY 61 LDANODEQVDFEFTSLVAIALKAHHTHKE 92
 DB 61 LDANODEQVDFEFTSLVAIALKAHHTHKE 92

IT 2

calgranulin c - pig

C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 23-May-1997

C:Accession: A55406

R:Del1:Angelica, E.C.; Schleicher, C.H.; Santone, J.A.

J. Biol. Chem. 269, 28929-28936, 1994

A:Title: Primary structure and binding properties of calgranulin C, a novel S100-like ca

A:Reference number: A55406; M01D:95050708

A:Accession: A55406

A>Status: preliminary

A:Molecule type: protein

C:Superfamily: S-100 protein; calmodulin repeat homology

C:Keywords: calcium binding; EF hand

F:48-80/Domain: calmodulin repeat homology <EF2>

Query Match 70.9%; Score 332; DB 2; Length 91;
 Best Local Similarity 70.3%; Pred. No. 3e-23;
 Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

OY 2 TKLEHLEGIIVNIFHOYSVRKGHFDPLSKGELKOLLTELANTIKNKRAVIDEIFOG 61
 DB 1 TKLEHLEGIIVNIFHOYSVRKGHFDPLSKGELKOLLTELANTIKNKRAVIDEIFOG 60

OY 62 DANODEQVDFEFTSLVAIALKAHHTHKE 92
 DB 62 DANODEQVDFEFTSLVAIALKAHHTHKE 92

61 DANODEQVDFEFTSLVAIALKAHHTHKE 91

RESULT 3

A42628

calgranulin B - bovine (fragment)

N:Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997

C:Accession: B22309; A42628

R:Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen,

submitted to the Protein Sequence Database, July 1992

A:Reference number: A22309

A:Accession: B22309

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-122 <78N>

R:Danoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignals, P.V.

Biochemistry 31, 5898-5905, 1992

A:Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil

A:Reference number: A42628; M01D:92304974

A:Accession: A42628

A:Molecule type: protein

A:Residues: 4-32, 'F', 34-56 <DIA>
 C:Complex: heterodimer and higher complexes with calgranulin A
 C:Superfamily: S-100 protein; calmodulin repeat homology
 C:Keywords: blocked amino end; calcium binding; EF hand; heterodimer; inflammation;
 F:6-40/Domain: calmodulin repeat homology <EF1>
 F:50-82/Domain: calmodulin repeat homology <EF2>

Query Match 48.4%; Score 226.5; DB 1; Length 122;
 Best Local Similarity 51.6%; Pred. No. 1.2e-13;
 Matches 47; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGHFDPLSKGELKOLLTELANTIKNKRAVIDEIFOG 59
 DB 1 MSOMESSIEFTIINIFHOYSVRGLHFDPLSKGELKOLLTELANTIKNKRAVIDEIFOG 60

OY 60 GLDANODEQVDFEFTSLVAIALKAHHTHKE 90
 DB 61 DLDNDVKQLSFEFTSLVAIALKAHHTHKE 91

RESULT 4

B31848

calgranulin B [validated] - human

N:Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antipe

(MRP-14); MIF-related 14K protein; S-100 calcium-binding protein A9 (S100A9)

C:Species: Homo sapiens (man)

C:Date: 21-May-1990 #sequence_revision 23-May-1997 #text_change 08-Dec-2000

C:Accession: B31848; S00667; A33819; B60911; B61082; D54327

R:Agasse, E.; Clerc, R.G.;

Mol. Cell. Biol. 8, 2402-2410, 1988

A:Title: Cloning and expression of two human genes encoding calcium-binding protein

A:Reference number: A93102; M01D:88302148

A:Accession: B31848

A:Molecule type: DNA

A:Residues: 1-114 <CAG>

A:Cross-references: GB:M21064; NID:918689; PIDN:AAA6326.1; PID:9386958

R:Odink, K.; Cerletti, N.; Brueggem, J.; Clerc, R.G.; Tarsesay, L.; Zwadlo, G.; Gerh

Nature 330, 80-82, 1987

A:Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthr

A:Reference number: S00667; M01D:88039099

A:Accession: S00667

A:Molecule type: mRNA

A:Residues: 1-114 <CAG>

A:Cross-references: EMBL:X06233; NID:934770; PIDN:CAA29579.1; PID:934771

A:Note: parts of this sequence were confirmed by protein sequencing

R:Murro, S.; Collart, F.R.; Huberman, E.

J. Biol. Chem. 264, 8356-8360, 1989

A:Title: A protein containing the cystic fibrosis antigen is an inhibitor of protei

A:Reference number: A33819; M01D:8925276

A:Accession: A33819

A:Molecule type: mRNA

A:Residues: 1-114 <MUR>

A:Cross-references: GB:M26111; NID:986219; PIDN:AAA68480.1; PID:9516621

A:Note: part of this sequence was confirmed by protein sequencing; the amino end of

R:Andersen, K.B.; Sletten, K.; Berntzen, H.B.; Dale, I.; Brandtzeig, P.; Jellum, E

Scand. J. Immunol. 28, 241-245, 1988

A:Title: The leucocyte IL protein: identity with the cystic fibrosis antigen and th

A:Reference number: A60911; M01D:88321575

A:Accession: B60911

A:Molecule type: protein

A:Residues: 39-42, 'X', 44-50, 64-77, 'X', 79, 84, 'X', 86-90, 'X', 92-94, 'X', 96-98 <AND>

R:Obbe, T.; Murakami, K.; Tomita, M.; Nozawa, R.

Chem. Pharm. Bull. 37, 1576-1580, 1989

A:Title: Amino acid sequences of 6088 antigens induced in HL-60 cells by 1,25-dihyd

A:Reference number: A61082; M01D:89376638

A:Accession: B61082

A:Molecule type: protein

A:Residues: 5-77, 80-90, 'A', 92-114 <NOB>

A:Note: the blocked amino end of the mature protein is identified as 2-Thr; residue

R:Andersen, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; K

J. Invest. Dermatol. 97, 701-712, 1991

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 8, 2001, 15:03:05 ; Search time 14.33 Seconds

(without alignments)
441.208 Million cell updates/sec

Title: US-09-227-854-2

Sequence: 1 MKRLKEHLEGIYVIFHQYSV.....EFISLVALKKAHYTHKE 92

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 198801 seqs, 68722935 residues

11 number of hits satisfying chosen parameters: 198801

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.67:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	468	100.0	92	2	JC4712
2	332	70.9	91	2	A55406
3	226.5	48.4	122	1	A42628
4	214.5	45.8	114	1	B31848
5	194	41.5	95	2	S24146
6	190	40.6	92	2	A48015
7	189	40.4	92	1	BCB01B
8	187	40.0	92	2	A26557
9	185	39.5	91	1	BCB01B
10	180.5	38.6	113	1	JN0686
11	178.5	38.1	113	1	S68242
12	177.5	37.9	95	1	S35985
13	167	35.9	591	2	A45135
14	166	35.7	102	1	JQ1300
15	163.5	34.9	101	2	S06207
16	162.5	34.7	94	1	BCB01A
17	161.5	34.5	94	1	BCB01A
18	160.5	34.3	101	2	S01759
19	158	33.8	93	1	BCB01C
20	157.5	33.7	101	2	A48219
21	157	33.5	105	1	I37080
22	156	33.3	306	2	A48118
23	154	32.9	89	1	I56163
24	153.5	32.8	98	2	A41988
25	152.5	32.6	100	2	A53217
26	149	31.8	89	1	JN0685
27	147.5	31.5	90	1	BCB01C
28	147.5	31.5	97	2	A30129
29	146	31.2	110	2	B48219

30	144.5	30.9	217	2	JN0330	26-kDa Ca2+-bindin
31	142.5	30.4	89	2	A54314	calyculin - mouse
32	142.5	30.4	90	1	S27011	calyculin - rabbit
33	139.5	29.8	90	2	B28363	calyculin - rat
34	139	29.7	99	2	S20342	calyculin-binding pr
35	137.5	29.4	98	2	JC5064	S-100 calcium-bind
36	136	29.1	65	2	A41004	calyculin - chic
37	127.5	27.2	95	1	LUPG10	calyculin I light
38	127.5	27.2	97	1	JH0663	calyculin I light
39	127.5	27.2	97	2	JC1139	calyculin I light
40	127.5	27.0	97	2	B28489	calyculin I light
41	126.5	27.0	97	2	A28489	calyculin I light
42	124	26.5	79	1	KLBO1	calyculin-binding pr
43	123.5	26.4	95	2	A31373	calyculin I light
44	122.5	26.2	79	1	KLPG1	calyculin-binding pr
45	121.5	26.0	79	1	JN0246	calyculin-binding pr

ALIGNMENTS

RESULT 1
JC4712
S-100 calcium-binding protein A12 - human
N:Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; utrophin protein
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence, revision 19-Jul-1996 #text_change 13-Aug-1999
C:Accession: JC4712; JC4717; JC4891; S56113; S56114
R:Yamamura, T.; Hittomi, J.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Salto, S.; Tsu
Biochem. Biophys. Res. Commun. 221, 356-360, 1996
A:Title: Human CAAF1 gene - molecular cloning, gene structure, and chromosome mappl
A:Reference number: JC4712; MUID:96192053
A:Accession: JC4712
A:Molecule type: mRNA
A:Residues: 1-92 <YAM>
A:Cross-references: DDBJ:DB3657; NID:G1502284; PIDN:BAI12030.1; PID:G1502285
R:Maril, T.; Ertmann, K.D.; Gallin, M.Y.
Biochem. Biophys. Res. Commun. 221, 454-458, 1996
A:Title: Host-parasite interaction in human onchocerciasis: Identification and sequ
A:Reference number: JC4717; MUID:96192069
A:Accession: JC4717
A:Molecule type: protein
A:Residues: 2-92 <MAR>
A:Experimental source: Onchocerca volvulus infecting human tissue
R:Ilig, E.C.; Troxler, H.; Buergisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.;
Biochem. Biophys. Res. Commun. 225, 146-150, 1996
A:Title: Amino acid sequence determination of human S100 A12 (p6, Calgranulin C, CG
A:Reference number: JC4891; MUID:96352419
A:Accession: JC4891
A:Molecule type: protein
A:Residues: 2-92 <ILG>
R:Guignard, F.; Manuel, J.; Markert, M.
Biochem. J. 309, 395-401, 1995
A:Title: Identification and characterization of a novel human neutrophil protein re
A:Reference number: S56113; MUID:95351965
A:Accession: S56113
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 'XX', 4-14, 'Y', 16-17, 'XXX', <GUI>
A:Experimental source: Isoform 6a
A:Accession: S56114
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 2-21 <GUI2>
A:Experimental source: Isoform 6b
C:Comment: This protein is released by activated neutrophils in the course of infla
C:Gene: GDB:S100A12; p6; MRP6; CGP; CAAF1
A:Cross-references: GDB:S5218374
A:Map position: 1q21-1q21
C:Complex: monomer
C:Superfamily: S-100 protein; calmodulin repeat homology

RX MEDLINE-85291729; PubMed-4031854;
 RA Jensen R., Marshak D.R., Anderson C., Lukas T.J., Matterson D.M.;
 RT "Characterization of human brain S100 protein fraction: amino acid
 sequence of S100 beta";
 RL J. Neurochem. 45:700-705(1985);
 RN (3)
 RP METAL ION-BINDING PROPERTIES.
 RA MEDLINE-85023393; PubMed-6487634;
 RX Baudier J., Glasser N., Haglid K., Gerard D.;
 RT "Purification, characterization and ion binding properties of human
 brain S100b protein";
 RL Biochim. Biophys. Acta 790:164-173(1984).
 RN (4)
 RP STRUCTURE BY NMR.
 RA MEDLINE-98179937; PubMed-9519411;
 RX Smith S.P., Shaw G.S.;
 RT "A novel calcium-sensitive switch revealed by the structure of human
 S100b in the calcium-bound form";
 RL Structure 6:211-222(1998).
 CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
 DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
 IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
 ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
 AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
 ONE ALPHA AND ONE BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
 BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
 CC -1- MISCELLANEOUS: IN ADDITION TO METAL-ION BINDING, THIS PROTEIN IS
 INVOLVED WITH THE REGULATION OF PROTEIN PHOSPHORYLATION IN BRAIN
 TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC
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 DR EMBL; M59488; AAA60367.1; -
 DR EMBL; M59487; AAA60367.1; JOINED.
 DR PIR; A03076; BCHUB.
 DR PIR; A38364; A38364.
 DR PDB; 1UWO; 10-JUN-98.
 DR MIM; 176990; -
 DR InterPro: IPR001751; -
 DR InterPro: IPR002048; -
 DR Pfam: PF01023; S.100; 1.
 DR Pfam: PF00036; efhand; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00303; S100_CAMP; 1.
 DR Calcium-binding; zinc; Metal-binding; 3D-structure.
 RT INT MET 0
 FT MOD RES 1 1 BLOCKED.
 FT CA_BIND 18 31 SITE I (LOW AFFINITY).
 FT CA_BIND 61 72 SITE II (HIGH AFFINITY).
 SQ SEQUENCE 91 AA; 10582 MW; 2378AAB8BFEA9F6 CRC64;

Query Match 39.3%; Score 184; DB 1; Length 91;
 Best Local Similarity 38.8%; Pred. No. 4.7e-11;
 Matches 33; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

Oy 2 TKLEHLEGIYINIFHOVSVRKGFHPTLSKGLKOLLTKELANTIKINIKRAVIDEIOGL 61
 Db 1 SELEKAMALLDVFHYGSRGDKHKLKSLKELINNELSHPLEINEGEVAVKMETL 60
 Oy 62 DANODEVDFEFTSLVAIALKAH 86

Db 61 DNDGDECDPQEFMAFVAMVTACH 85
 RESULT 14
 ID S10B_RAT STANDARD: PRT: 91 AA.
 AC P04651;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE S-100 PROTEIN, BETA CHAIN.
 GN S100B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid-10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-85037924; PubMed-6093041;
 RA Kuwano R., Usui H., Maeda T., Fukui T., Yamamori N., Ohtsuka E.,
 RA Ikehara M., Takahashi Y.;
 RT "Molecular cloning and the complete nucleotide sequence of cDNA to
 mRNA for s-100 protein of rat brain";
 RL Nucleic Acids Res. 12:7455-7465(1984).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Kuwano R., Usui H., Maeda T., Araki K., Kurihara T., Yamakuni T.,
 RA Ohtsuka E., Ikehara M., Takahashi Y.;
 RT "Molecular cloning and nucleotide sequences of cDNA and genomic DNA
 for alpha and beta subunits of S100 protein";
 RL Tanaguchi Symp. Brain Sci. 19:243-255(1987).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91359841; PubMed-1653388;
 RA Maeda T., Usui H., Araki K., Kuwano R., Takahashi Y., Suzuki Y.;
 RT "Structure and expression of rat S-100 beta subunit gene";
 RL Brain Res. Mol. Brain Res. 10:193-202(1991).
 RN (4)
 RP SEQUENCE OF 5-91 FROM N.A.
 RX MEDLINE-87137648; PubMed-3818655;
 RA Dunn R., Landry C., O'Hanlon D., Dunn J., Alliore R., Brown I.,
 RA Marks A.;
 RT "Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells
 following treatment with anti-microtubular drugs";
 RL J. Biol. Chem. 262:3562-3566(1987).
 RN (5)
 RP STRUCTURE BY NMR.
 RX MEDLINE-96387197; PubMed-8794737;
 RA Drohat A.C., Amburgey J.C., Abildgaard F., Starich M.R.,
 RA Baldisseri D.M., Weber D.J.;
 RT "Solution structure of rat apo-S100B(beta beta) as determined by NMR
 spectroscopy";
 RL Biochemistry 35:11577-11588(1996).
 RN (6)
 RP STRUCTURE BY NMR.
 RX MEDLINE-98153156; PubMed-9485423;
 RA Drohat A.C., Baldisseri D.M., Rustandi R.R., Weber D.J.;
 RT "Solution structure of calcium-bound rat S100B(beta beta) as
 determined by nuclear magnetic resonance spectroscopy";
 RL Biochemistry 37:2729-2740(1998).
 RN (7)
 RP STRUCTURE BY NMR.
 RX MEDLINE-99226808; PubMed-10211826;
 RA Drohat A.C., Tjandra N., Baldisseri D.M., Weber D.J.;
 RT "The use of dipolar couplings for determining the solution structure
 of rat apo-S100b";
 RL Protein Sci. 8:800-809(1999).
 CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY-
 DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
 IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
 ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
 AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
 CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR

RT "Spectral studies on the cadmium-ion-binding properties of bovine
RT brain S-100b protein.";
RL Biochem. J. 276:13-18(1991).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE-96398693; PubMed-8805590;
RA Kildy P.M., van Eldik L.J., Roberts G.C.K.;
RT "The solution structure of the bovine S100b protein dimer in the
RT calcium-free state."
CC Structure 4:1041-1052(1996).
CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY.
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC ONE ALPHA AND ONE BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC PIR: A03077; BCB01B.
CC PDB: ICFP; 12-MAR-97.
CC PDB: IMHO; 18-NOV-98.
CC InterPro: IPR001751;
CC InterPro: IPR002048;
CC DR Pfam: PF01023; S.100; 1.
CC DR Pfam: PF00036; ehand; 1.
CC DR PROSITE: PS00018; EF_HAND; 1.
CC DR PROSITE: PS00303; S100_CABP; 1.
CC KW Calcium-binding; zinc; Metal-binding; Acetylation; 3D-structure.
CC FT MOD_RES 1 1 ACETYLATION
CC FT CA_BIND 18 31 SITE I (LOW AFFINITY).
CC FT CA_BIND 61 72 SITE II (HIGH AFFINITY).
CC FT SEQUENCE 91 AA: 10537 MW: 386201933DEB93A CRC64;
SQ

Query Match 39.5%; Score 185; DB 1; Length 91;
Best Local Similarity 38.8%; Pred. No. 3.8e-11;
Matches 33; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

QY 2 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTFELANTIKINIKDKAVIDEIPOOL 61
DB 1 SELEKAVALLIDVPHOYSGREGDKRKLKSELKELINNELSHLEIKOEVDKVMETL 60
QY 62 DANODEQVDFQEFISLVAIALKAH 86
DB 61 DSDGDGECDFQEFMAFVAMVTACH 85

RESULT 12
S10B_MOUSE
ID S10B_MOUSE STANDARD; PRT; 91 AA.
AC P50114;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE S-100 PROTEIN, BETA CHAIN.
GN S100B.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN-BALB/C;
RX MEDLINE-93386628; PubMed-8376406;
RA Jiang H., Shah S., Hilt D.C.;
RT "Organization, sequence, and expression of the murine S100 beta gene.
RT Transcriptional regulation by cell type-specific cis-acting
RT regulatory elements."
RL J. Biol. Chem. 268:20502-20511(1993).

CC -1- FUNCTION: WEAKLY BINDS CALCIUM BUT BINDS ZINC VERY TIGHTLY.
CC DISTINCT BINDING SITES WITH DIFFERENT AFFINITIES EXIST FOR BOTH
CC IONS ON EACH MONOMER. PHYSIOLOGICAL CONCENTRATIONS OF POTASSIUM
CC ION ANTAGONIZE THE BINDING OF BOTH DIVALENT CATIONS, ESPECIALLY
CC AFFECTING HIGH-AFFINITY CALCIUM-BINDING SITES.
CC -1- SUBUNIT: DIMER OF EITHER TWO ALPHA CHAINS, OR TWO BETA CHAINS, OR
CC ONE ALPHA AND ONE BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: ALTHOUGH PREDOMINANT AMONG THE WATER-SOLUBLE
CC BRAIN PROTEINS, S-100 IS ALSO FOUND IN A VARIETY OF OTHER TISSUES
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
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CC
CC EMBL: L22144; AAA03075.1;
CC DR HSSP: P04271; 1U00.
CC DR MGP: MGI:98217; S100b.
CC InterPro: IPR001751;
CC InterPro: IPR002048;
CC DR Pfam: PF01023; S.100; 1.
CC DR Pfam: PF00036; ehand; 1.
CC DR PROSITE: PS00018; EF_HAND; 1.
CC DR PROSITE: PS00303; S100_CABP; 1.
CC KW Calcium-binding; zinc; Metal-binding;
CC FT INIT_MET 0 0 BY SIMILARITY
CC FT CA_BIND 18 31 SITE I (LOW AFFINITY).
CC FT CA_BIND 61 72 SITE II (HIGH AFFINITY).
CC FT SEQUENCE 91 AA: 10597 MW: 2378A8B8BE1C94D CRC64;
SQ

Query Match 39.5%; Score 185; DB 1; Length 91;
Best Local Similarity 38.8%; Pred. No. 3.8e-11;
Matches 33; Conservative 26; Mismatches 26; Indels 0; Gaps 0;

QY 2 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTFELANTIKINIKDKAVIDEIPOOL 61
DB 1 SELEKAVALLIDVPHOYSGREGDKRKLKSELKELINNELSHLEIKOEVDKVMETL 60
QY 62 DANODEQVDFQEFISLVAIALKAH 86
DB 61 DSDGDGECDFQEFMAFVAMVTACH 85

RESULT 13
S10B_HUMAN
ID S10B_HUMAN STANDARD; PRT; 91 AA.
AC P04271;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE S-100 PROTEIN, BETA CHAIN.
GN S100B.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE-90368757; PubMed-2394738;
RA Alloue R.J., Friend W.C., O'Hanlon D., Neilson K.M., Bauman R.,
RA Dunn R.J., Marks A.;
RT "Cloning and expression of the human S100 beta gene."
RT J. Biol. Chem. 265:15537-15543(1990).
RN [2]
RP SEQUENCE.

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CC -----
 DR EMBL: X65614; CAA46566.1; -
 DR PIR: S24146; S24146.
 DR HSP: P02638; ICNP.
 DR MIM: 600614; -
 DR InterPro: IPR001751; -
 DR InterPro: IPR002048; -
 DR Pfam: PF01023; S.100; 1.
 DR Pfam: PF00036; eHand; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR Calcium-binding; Placenta.
 DR CA_BIND 19 32 SITE I (LOW AFFINITY).
 FT CA_BIND 62 73 SITE II (HIGH AFFINITY).
 FT CONFLICT 32 32 E -> T (IN REF. 2).
 FT CONFLICT 44 44 F -> E (IN REF. 2).
 J SEQUENCE 95 AA; 10400 MW; 786B6E3FEAC6C1 CRC64;

Query Match 41.5%; Score 194; DB 1; Length 95;
 Best Local Similarity 45.1%; Pred. No. 5.7e-12;
 Matches 41; Conservative 17; Mismatches 33; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIWNIHFQSVYRKGFDTLSKGLKQLTKELANTIKNIKDAVIDEFG 60
 DB 1 MTELETAMGMIIIVFSRSYSGESTOTLTGKELKMLPELGLGKDKDAVDKLLKD 60
 OY 61 LDANODEVDYDFEFISLVAIALKAHYTHK 91
 DB 61 LDANGDQVDYDFEFISLVAIALKAHYTHK 91

RESULT 10
 ID S101_ICTPU STANDARD; PRT; 92 AA.

AC 091061;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ICMACALCIN.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Siluriformes; Ictaluridae; Ictalurus.
 NCBI_TaxID=7998;

SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=97038343; PubMed=883937;
 RA Porta A.R., Bettini E., Bulakova O.I., Baker H., Danho W.,
 RA Margolis F.L.;
 RT "Molecular cloning of Ictacalcin: a novel calcium-binding protein
 RT from the channel catfish, Ictalurus punctatus";
 RL Brain Res. Mol. Brain Res. 41:81-89(1996).
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN CATFISH CALCIUM HOMEOSTASIS.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN EPITHELIAL CELLS OF OLFACTORY
 CC ROSETTE, BARBEL, SKIN AND GILL BUT NOT BRAIN OR MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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DR EMBL: U33273; AAB52610.1; -
 DR HSP: P30801; ICNP.
 DR InterPro: IPR001751; -
 DR InterPro: IPR002048; -
 DR Pfam: PF01023; S.100; 1.
 DR Pfam: PF00036; eHand; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR Calcium-binding.
 DR CA_BIND 19 32 SITE I (LOW AFFINITY) (POTENTIAL).
 FT CA_BIND 62 73 SITE II (HIGH AFFINITY) (POTENTIAL).
 FT CONFLICT 32 32 E -> T (IN REF. 2).
 FT CONFLICT 44 44 F -> E (IN REF. 2).
 SQ SEQUENCE 92 AA; 10021 MW; DBFE786B7F921C58 CRC64;

Query Match 40.2%; Score 188; DB 1; Length 92;
 Best Local Similarity 46.8%; Pred. No. 2e-11;
 Matches 37; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIWNIHFQSVYRKGFDTLSKGLKQLTKELANTIKNIKDAVIDEFG 60
 DB 1 MSDLQGMALLISTFHKYSGKEDKCTLTGKELKMLPELGLGKDKDAVDKLLKD 60
 OY 61 LDANODEVDYDFEFISLVA 79
 DB 61 LDNADGVVDYDFEFISLVA 79

RESULT 11
 ID S10B_BOVIN STANDARD; PRT; 91 AA.

AC P02638;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE S-100 PROTEIN, BETA CHAIN.
 GN S100B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;

SEQUENCE
 RX MEDLINE=79045265; PubMed=710399;
 RA Isobe T., Okuyama T.;
 RT "The amino-acid sequence of S-100 protein (PAP I-b protein) and its
 RT relation to the calcium-binding proteins";
 RL Eur. J. Biochem. 89:379-386(1978).
 RN [2]
 RP REVISIONS TO 1-4.
 RX MEDLINE=81236562; PubMed=7250124;
 RA Isobe T., Okuyama T.;
 RT "The amino-acid sequence of the alpha subunit in bovine brain S-100a
 RL Eur. J. Biochem. 116:79-86(1981).
 RN [3]

SEQUENCE
 RX MEDLINE=85278169; PubMed=4026304;
 RA Marshak D.R., Umekawa H., Watterson D.M., Hidaka H.;
 RT "Structural characterization of the calcium binding protein S100 from
 RT adipose tissue";
 RL Arch. Biochem. Biophys. 240:777-780(1985).
 RN [4]
 RP METAL ION-BINDING PROPERTIES.
 RX MEDLINE=84000339; PubMed=6615778;
 RA Baudier J., Gerard D.;
 RT "Ions binding to S100 proteins: structural changes induced by calcium
 RT and zinc on S100a and S100b proteins";
 RL Biochemistry 22:3360-3369(1983).
 RN [5]
 RP CADMIUM-BINDING STUDIES.
 RX MEDLINE=91248136; PubMed=2039467;
 RA Donato H. Jr., Mani R.S., Kay C.M.;

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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X61200; NOT_ANNOTATED_CDS.
DR HSSP: P04271; LUMO.
DR InterPro: IPR001751; .
DR InterPro: IPR002048; .
DR Pfam: PF01023; S_100; 1.
DR Pfam: PF00036; ehand; 1.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
DR Calcium-binding.
DR CA_BIND 29 42 SITE I (LOW AFFINITY) (POTENTIAL).
DR CA_BIND 72 83 SITE II (HIGH AFFINITY) (POTENTIAL).
DR SEQUENCE 119 AA; 14065 MW; 2D268DAF6309AD7A CRC64;
SQ
Query Match 44.9%; Score 210; DB 1; Length 119;
Best Local Similarity 43.3%; Pred. No. 2,3e-13;
Matches 39; Conservative 26; Mismatches 25; Indels 0; Gaps 0;
OY 1 MKLEHEGIVNIFPHQSVRKGHDTLSKGLKLTKELENTININDKVIDEIRFG 60
Db 11 LSELEKADVIITDFHQSRREGDKDTLRKEKLTLEKOLANYLKHVNOVSIDIFND 70
OY 61 LDANODEVDFQEFISLVAIALKAHYH7H 90
Db 71 LDNNKDDQSLFGEVMLIRVTVATHEHLH 100
RESULT 8
S109_RABIT STANDARD; PRT; 118 AA.
ID S109_RABIT
AC P50117;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CALGRAULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
DE (MRP-14) (FRAGMENT).
GN S100A9 OR MRP-14.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
AP [1]
NP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils;
RX MEDLINE=9635278; PubMed=8702688;
RA Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J.,
RA Underwood J.R., Robinson H.C.;
RA "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-
RT calgranulin C when incubated with inorganic [35S]sulfate";
RL J. Biol. Chem. 271:19802-19809(1996).
RN [2]
RP SEQUENCE OF 45-82 FROM N.A.
RC STRAIN-NEW ZEALAND WHITE;
RX MEDLINE=94198229; PubMed=8148323;
RA Mori S., Goto K., Goto F., Mutakami K., Okawara S., Yoshinaga M.;
RA "Dynamic changes in mRNA expression of neutrophils during the course
RT of acute inflammation in rabbits.";
RL Int. Immunol. 6:149-156(1994).
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL: AF091849; AAC61771.1; .
DR EMBL: D17404; BAA04227.1; .
DR InterPro: IPR001751; .
DR InterPro: IPR002048; .
DR InterPro: IPR002395; .
DR Pfam: PF01023; S_100; 1.
DR Pfam: PF00036; ehand; 1.
DR PRINTS: PR00334; KINNOGEN.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00303; S100_CABP; 1.
DR Calcium-binding; Repeat.
DR NON_TER 1 1
DR CA_BIND 9 22 SITE I (LOW AFFINITY) (POTENTIAL).
DR CA_BIND 53 64 SITE II (HIGH AFFINITY) (POTENTIAL).
DR DOMAIN 103 118 2 x 8 AA TANDEM REPEATS OF G-H-G-H-
G-H-S-H.
DR REPEAT 103 110 1.
DR REPEAT 111 118 2.
DR SEQUENCE 118 AA; 13292 MW; 7496118E21AD5C41 CRC64;
SQ
Query Match 43.1%; Score 201.5; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 1,4e-12;
Matches 41; Conservative 17; Mismatches 23; Indels 1; Gaps 1;
OY 11 IVNIFHQSVRKGHDTLSKGLKLTKELENTI-KNIKDAVIDEIRFGDANODECV 69
Db 1 IINIFHQSVRKGHDTLSKGLKLTKELENTI-KNIKDAVIDEIRFGDANODECV 60
OY 70 DFOEFISLVAIALKAHYH7H 91
Db 61 SFEFEVILMARLVHSHHEMRK 82
RESULT 9
S10E_HUMAN STANDARD; PRT; 95 AA.
ID S10E_HUMAN
AC P25815;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE S-100P PROTEIN.
GN S100P OR S100E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
AP [1]
NP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=92339442; PubMed=1633809;
RA Becker T., Gerke V., Kube E., Weber K.;
RA "S100P, a novel Ca(2+)-binding protein from human placenta. cDNA
RT cloning, recombinant protein expression and Ca2+ binding
RT properties";
RL Eur. J. Biochem. 207:541-547(1992).
RN [2]
RP SEQUENCE OF 1-91.
RC TISSUE-Placenta;
RX MEDLINE=92171935; PubMed=1540168;
RA Emoto Y., Kobayashi R., Akatsuka H., Hida H.;
RA "Purification and characterization of a new member of the S-100
RT protein family from human placenta.";
RL Biochem. Biophys. Res. Commun. 182:1246-1253(1992).
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS TWO CALCIUM IONS.
CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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DB 61 DLDTNADKOLSEEFETMLVARLTWASHEKHE 91

RESULT 6

ID S109_HUMAN STANDARD: PRT: 114 AA.

AC P06702;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)

DE (MRP-14) (P14) (LEUKOCYTE LI COMPLEX HEAVY CHAIN) (S100 CALCIUM-BINDING PROTEIN A9).

GN S100A9 OR MRP14 OR CAGB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

PP SEQUENCE FROM N.A.

MEDLINE=88039099; PubMed=3313057;

RA Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarcsay L., Zvaldo G., Gerhards G., Schlegel R., Sorg C.;

RT "Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis.";

RL Nature 330:80-82(1987).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=88302148; PubMed=3405210;

RA Lagasse E., Clerc R.G.;

RT "Cloning and expression of two human genes encoding calcium-binding proteins that are regulated during myeloid differentiation.";

RL Mol. Cell. Biol. 8:2402-2410(1988).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=89255276; PubMed=2656677;

RA Murao S., Collart F.R., Huberman E.;

RT "A protein containing the cystic fibrosis antigen is an inhibitor of protein kinases.";

RL J. Biol. Chem. 264:8356-8360(1989).

RN [4]

RP SEQUENCE FROM N.A.

RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;

RT "Human gene for migration inhibitory factor-related protein 14 (MRP14), variant allele.";

RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RP [5]

RP SEQUENCE OF 84-114, AND PHOSPHORYLATION.

RX MEDLINE=90044075; PubMed=2478889;

RA Edgeworth J., Freeman P., Hogg N.;

RT "Ionomycin-regulated phosphorylation of the myeloid calcium-binding protein p14.";

RL Nature 342:189-192(1989).

RN [6]

RP SEQUENCE OF 11-19; 26-37 AND 94-107.

RX MEDLINE=93162043; PubMed=1286662;

RA Rasmussen H.H., van Damme J., Puye M., Gesser B., Cells J.E., Vandekerckhove J.;

RT "Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";

RL Electrophoresis 13:960-969(1992).

CC -1- FUNCTION: EXPRESSED BY MACROPHAGES IN ACUTELY INFLAMMATED TISSUES AND IN CHRONIC INFLAMMATIONS. SEEM TO BE AN INHIBITOR OF PROTEIN KINASES. ALSO EXPRESSED IN EPITHELIAL CELLS CONSTITUTIVELY OR INDUCED DURING DERMATOSES. MAY INTERACT WITH COMPONENTS OF THE INTERMEDIATE FILAMENTS IN MONOCYTES AND EPITHELIAL CELLS.

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC -----

CC EMBL: X06233; CAA29579.1; -

CC EMBL: M21064; AAA36326.1; -

CC EMBL: M26311; AAA68480.1; -

CC EMBL: AF237581; AAF62536.1; -

CC EMBL: A12032; CAA01002.1; -

CC EMBL: A12032; CAA01004.1; -

CC PIR: B31848; B31848.

CC PIR: A33819; A33819.

CC HSSP: P02638; 1CFP.

CC Aairhus/Ghent-2DPAGE; 5007; IEF.

CC Aairhus/Ghent-2DPAGE; 6010; IEF.

CC Aairhus/Ghent-2DPAGE; 6017; IEF.

CC Aairhus/Ghent-2DPAGE; 7013; IEF.

CC MIM: 123886; -

CC InterPro: IPR001751; -

CC InterPro: IPR002048; -

CC Pfam: PF01023; S_100; 1.

CC Pfam: PF00036; ehnd; 1.

CC PROSITE: PS00018; EF_HAND; 1.

CC PROSITE: PS00303; S100_CABP; 1.

CC K2 Calcium-binding; Macrophage; Phosphorylation.

CC FT CA_BIND 23 36 SITE I (LOW AFFINITY) (POTENTIAL).

CC FT CA_BIND 67 78 SITE II (HIGH AFFINITY) (POTENTIAL).

CC MOD_RES 113 113 PHOSPHORYLATION.

CC SEQ SEQUENCE 114 AA; 13242 MW; C3BE19729E14C078 CRC64;

Query Match 45.8%; Score 214.5; DB 1; Length 114;

Best Local Similarity 46.7%; Pred. No. 8.2e-14;

Matches 43; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

QY 1 MTKLEHLEGIWVIFPHQSVKGFPTLSKGLKLTKELANTI-KNIKRAVIDEIRQ 59

DB 5 MSGLERNIEITITFPHQSVKGLHPTDLNGEKEKELVRDQLGNFKENKNEVIEHWE 64

QY 60 GLDANODEQVDFQEFISLVAIALKAHYTHK 91

DB 65 DLDTNADKOLSEEFETMLVARLTWASHEKHE 96

RESULT 7

ID M126_CHICK STANDARD: PRT: 119 AA.

AC P28318;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PROTEIN MRP-126.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LEHORN; TISSUE-Bone marrow;

RX MEDLINE=92195690; PubMed=1549365;

RA Nakano T., Graf T.;

RT "Identification of genes differentially expressed in two types of v-myc-transformed avian myelomonocytic cells.";

RL Oncogene 7:527-534(1992).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN V-MYB-TRANSFORMED MYELOMONOCYTIC CELLS.

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.

CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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FT INIT MET 0 0 BY SIMILARITY.
 FT CA BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).
 FT CA BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 SO SEQUENCE 91 AA; 10554 MW; 66FBC3C1B0354482 CRC64;

Query Match 67.1%; Score 314; DB 1; Length 91;

Best Local Similarity 65.9%; Pred. No. 2.8e-23; Matches 60; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 2 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKIKDKAVIDEFOGL 61
 DB 1 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKIKDKAVIDEFOGL 60
 QY 62 DANODEQVDFEFLISVAIALKAHYHTHKE 92
 DB 61 DADKGAVSFEFVLVSVLKTAKHIDHKE 91

12. RABIT

12. RABIT STANDARD; PRT; 81 AA.

AC 15-JUL-1998 (Rel. 38, Created)
 DT 15-JUL-1998 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CALGRANULIN C (CAGC) (FRAGMENT).
 GN S100A12.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils;

MEDLINE=96355278; PubMed=8702688;

Yang Z., Devere M.J., Gardner E.E., Devenish R.J., Handley C.J., Underwood J.R., Robinson H.C.,

"Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-

calgranulin C when incubated with inorganic [35S]sulfate."

J. Biol. Chem. 271:19802-19809(1996).

-1 SIMILARITY: BELONGS TO THE S-100 FAMILY.

-1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

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CC EMBL; AF091848; AAC61770.1;
 DR InterPro: IPR001751;
 DR InterPro: IPR002048;
 DR Pfam: PF01023; S.100; 1.
 DR Pfam: PF00036; ehand; 1.
 DR PROSITE: PS00018; EF_HAND; 1.
 DR PROSITE: PS00303; S100_CABP; 1.
 DR Calcium-binding; 1.
 FT NON_TER 1 1
 FT CA_BIND 8 21
 FT CA_BIND 51 62
 FT SEQUENCE 81 AA; 9401 MW; 95E67A209180CB6 CRC64;

Query Match 58.3%; Score 273; DB 1; Length 81;

Best Local Similarity 64.2%; Pred. No. 1.8e-19; Matches 52; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 12 VNIFHOYSVRKGFDTLSKGLKQLTKELANTIKIKDKAVIDEFOGLDANODEQVDF 71
 DB 1 INIFHOYSVRKGFDTLSKGLKQLTKELANTIKIKDKAVIDEFOGLDANODEQVDF 60

QY 72 QEFISVAIALKAHYHTHKE 92
 DB 61 KEFLSLASVLTVAHENTHKE 81

RESULT 5

S109_BOVIN STANDARD; PRT; 122 AA.

AC P28783;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CALGRANULIN B (NEUTROPHIL CYTOSOLIC 23 KDA PROTEIN) (P23) (BEE22)
 GN S100A9.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;

SEQUENCE.

TISSUE=Esophageal epithelium.

MEDLINE=93280230; PubMed=8505358;

Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J., Wang M.-E., Chen L.B., Chen W.-T., Ip W., Lin D.C., Lin J.-C., Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.;

"Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal antibody W2 specifically reacts with condensed nuclei of differentiated superficial cells."

J. Cell Sci. 104:237-247(1993).

SEQUENCE OF 4-56.

TISSUE=Neutrophils;

MEDLINE=92304974; PubMed=1610833;

Dianoix A.-C., Stasia M.-T., Garin J., Gagnon J., Vignais P.V.;

"The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophil cytosol is a member of the S100 family."

Biochemistry 31:5898-5905(1992).

-1 SUBUNIT: DISULFIDE LINKED HETERODIMER OF A 7/11 KDA AND A 22/23 KDA SUBUNITS.

-1 SUBCELLULAR LOCATION: CYTOPLASMIC; LOOSELY ASSOCIATED TO THE CYTOSKELETON.

-1 TISSUE SPECIFICITY: FOUND ESSENTIALLY IN PHAGOCYTTIC CELLS.

-1 PFM: PHOSPHORYLATED BY PROTEIN KINASE C.

-1 MISCELLANEOUS: CONTAINS TWO CA(2+)-BINDING DOMAINS PER PROTEIN.

-1 SIMILARITY: BELONGS TO THE S-100 FAMILY.

-1 SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.

HSP; P02636; ICFP.

InterPro: IPR001751;

InterPro: IPR002048;

Pfam: PF01023; S.100; 1.

Pfam: PF00036; ehand; 1.

PROSITE: PS00018; EF_HAND; PARTIAL.

PROSITE: PS00303; S100_CABP; 1.

Calcium-binding; Phosphorylation.

NON_TER 1 1

CA_BIND 19 32

CA_BIND 63 74

SEQUENCE 122 AA; 13673 MW; F3CA8C4880BECDC CRC64;

Query Match 48.8%; Score 228.5; DB 1; Length 122;

Best Local Similarity 51.6%; Pred. No. 4.3e-15; Matches 47; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKIKDKAVIDEFOGL 59
 DB 1 MSQESSIEIIVNIFHOYSVRKGFDTLSKGLKQLTKELANTIKIKDKAVIDEFOGL 60

CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 CC EMBL: X97859; CA66453.1; -
 CC EMBL: X98288; CA66934.1; JOINED.
 CC EMBL: X98289; CA66934.1; JOINED.
 CC EMBL: X98290; CA66934.1; JOINED.
 CC EMBL: X98289; CAB94792.1; -
 CC EMBL: X98290; CAB94792.1; JOINED.
 CC EMBL: D49549; BAA08497.1; -
 CC EMBL: D83664; BAA12036.1; -
 CC EMBL: D83657; BAA12030.1; -
 CC HSSP: P02633; 1BOD.
 CC MIM: 603112; -
 CC InterPro: IPR001751; -
 CC InterPro: IPR002048; -
 CC Pfam: PF01023; S_100; 1.
 CC Pfam: PF00036; ehand; 1.
 CC PROSITE: PS00018; EF_HAND; FALSE_NEG.
 CC PROSITE: PS00303; S100_CABP; 1.
 CC Calcium-binding; zinc; Metal-binding.
 CC INIT_MET 0
 CC CA_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).
 CC CA_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 CC SEQUENCE 91 AA; 10444 MW; 325685EA8695F6B7 CRC64;
 SQ
 Query Match 98.9%; Score 463; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2,7e-37;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKOLLTKELANTIKNKAVIDEIFQGL 61
 DB 1 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKOLLTKELANTIKNKAVIDEIFQGL 60
 QY 62 DANODEQVDFEFISLVATAKAAHYHTHKE 92
 DB 61 DANODEQVDFEFISLVATAKAAHYHTHKE 91
 LP 2
 PIG STANDARD; PRT; 91 AA.
 ID S112_PIG
 AC P80310;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CALGRANULIN C (CAGC).
 GN S100A12.
 OS Sus scrofa (Pig).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Granulocyte; PubMed-7961855;
 RX MEDLINE=95050708; Santome J.A.;
 RA Dell'Angelica E.C., Schleicher C.H., Santome J.A.;
 RT "Primary structure and binding properties of calgranulin C, a novel
 RT 100-kDa calcium-binding protein from pig granulocytes.";
 RL J. Biol. Chem. 269:28929-28936(1994).
 CC -1- TISSUE SPECIFICITY: FOUND ESSENTIALLY IN GRANULOCYTES WITH SMALL
 CC AMOUNTS FOUND IN LYMPHOCYTES.
 CC -1- MISCELLANEOUS: IN THE ABSENCE OF ZINC BINDS ONE CALCIUM ION PER
 CC MOLECULE, IN THE PRESENCE OF ZINC BINDS TWO CALCIUM IONS PER

CC MOLECULE.
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
 CC HSSP: P02632; 1CB1.
 CC InterPro: IPR001751; -
 CC InterPro: IPR002048; -
 CC Pfam: PF01023; S_100; 1.
 CC Pfam: PF00036; ehand; 1.
 CC PROSITE: PS00018; EF_HAND; FALSE_NEG.
 CC PROSITE: PS00303; S100_CABP; 1.
 CC Calcium-binding; zinc; Metal-binding.
 CC CA_BIND 18 31 SITE I (LOW AFFINITY) (BY SIMILARITY).
 CC CA_BIND 61 72 SITE II (HIGH AFFINITY) (BY SIMILARITY).
 CC SEQUENCE 91 AA; 10614 MW; B4204461432DFCB CRC64;
 SQ
 Query Match 70.9%; Score 332; DB 1; Length 91;
 Best Local Similarity 70.3%; Pred. No. 5,7e-25;
 Matches 64; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
 QY 2 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKOLLTKELANTIKNKAVIDEIFQGL 61
 DB 1 TKLEHLEGIIVNIFHOYSVRKRGHPTLSKGLKOLLTKELANTIKNKAVIDEIFQGL 60
 QY 62 DANODEQVDFEFISLVATAKAAHYHTHKE 92
 DB 61 DANODEQVDFEFISLVATAKAAHYHTHKE 91
 RESULT 3
 S112_BOVIN STANDARD; PRT; 91 AA.
 ID S112_BOVIN
 AC P79105;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CALGRANULIN C (CAGC) (CALCIUM-BINDING PROTEIN IN AMNIOTIC FLUID 1)
 DE (CAAF1).
 GN S100A12 OR CAAF1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oesophagus;
 RX MEDLINE=96298783; PubMed-8718672;
 RA Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,
 RA Nagasaki K.;
 RT "A novel calcium-binding protein in amniotic fluid, CAAF1: its
 RT molecular cloning and tissue distribution.";
 RL J. Cell Sci. 109:805-815(1996).
 CC -1- SIMILARITY: BELONGS TO THE S-100 FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D49548; BAA08496.1; -
 CC HSSP: P02633; 1BOD.
 CC InterPro: IPR001751; -
 CC InterPro: IPR002048; -
 CC Pfam: PF01023; S_100; 1.
 CC Pfam: PF00036; ehand; 1.
 CC PROSITE: PS00018; EF_HAND; FALSE_NEG.
 CC PROSITE: PS00303; S100_CABP; 1.
 CC Calcium-binding; zinc; Metal-binding.

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OM protein - protein search, using sw model
Run on: June 8, 2001, 15:03:05 ; Search time 9.57 Seconds
(without alignments)
329.311 Million cell updates/sec

Title: US-09-227-854-2
Perfect score: 468
Sequence: 1 MTKLEHLEGIVNIFHOXSV.....EFISVAIAKAAHYHTRKE 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 93435 seqs, 34255486 residues

1 number of hits satisfying chosen parameters: 93435
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463	98.9	91	1	S112_HUMAN
2	332	70.9	91	1	S112_PIG
3	314	67.1	91	1	S112_BOVIN
4	273	58.3	81	1	S112_RABIT
5	228.5	48.8	122	1	S109_BOVIN
6	214.5	45.8	114	1	S109_HUMAN
7	210	44.9	119	1	M126_CHICK
8	201.5	43.1	118	1	S109_RABIT
9	194	41.5	95	1	S10E_HUMAN
10	188	40.2	92	1	S10I_TCTPU
11	185	39.5	91	1	S10B_BOVIN
12	185	39.5	91	1	S10B_MOUSE
13	184	39.3	91	1	S10B_HUMAN
14	182	38.9	91	1	S10B_RAT
15	180.5	38.6	113	1	S109_RAT
16	178.5	38.1	112	1	S109_MOUSE
17	167	35.7	102	1	S11I_RABIT
18	164.5	35.1	93	1	S10A_RAT
19	164	35.0	101	1	S11I_CHICK
20	163.5	34.9	101	1	S104_MOUSE
21	162.5	34.7	93	1	S10A_BOVIN
22	161.5	34.5	93	1	S10A_HUMAN
23	160.5	34.3	101	1	S10A_RAT
24	158	33.8	93	1	S108_HUMAN
25	157.5	33.7	101	1	S104_HUMAN
26	157	33.5	105	1	S11I_HUMAN
27	155.5	33.2	93	1	S108_MOUSE
28	154	32.9	88	1	S108_MOUSE
29	153.5	32.8	97	1	S11I_MOUSE
30	152.5	32.6	100	1	S102_HUMAN
31	152.5	32.6	100	1	S104_BOVIN
32	149.5	31.9	92	1	S106_HORSE
33	149	31.8	88	1	S108_RAT

ALIGNMENTS

RESULT ID	1	S112_HUMAN	STANDARD:	PRT:	91 AA.
AC	P80511:				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	CALGRANULIN C (CAGC) (P6) (CGRP) (NEUTROPHIL S100 PROTEIN) (CALCIUM-BINDING PROTEIN IN AMNIOTIC FLUID 1) (CAAF1) (P6).				
GN	S100A12.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE-97138564; PubMed-9885590;				
RA	Wicki R., Marenholz I., Mischke D., Schaefer B.W., Heizmann C.W.;				
RT	"Characterization of the human S100A12 (calgranulin C, p6, CAAF1, CGRP) gene, a new member of the S100 gene cluster on chromosome 12q21."				
RT	Cell Calcium 20:459-464(1996).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE-96192053; PubMed-8619860;				
RA	Yamamura T., Hitomi J., Nagasaki K., Suzuki M., Takahashi E.,				
RA	Saito S., Tsukada T., Yamaguchi K.;				
RT	"Human CAAF1 gene -- molecular cloning, gene structure, and chromosome mapping."				
RT	Biochem. Biophys. Res. Commun. 221:356-360(1996).				
RL	[3]				
RN	SEQUENCE.				
RP	MEDLINE-96192069; PubMed-8619876;				
RA	Martl T., Ettmann K.D., Gallin M.Y.;				
RT	"Host-parasite interaction in human onchocerciasis: Identification and sequence analysis of a novel human calgranulin C."				
RT	Biochem. Biophys. Res. Commun. 221:454-458(1996).				
RL	[4]				
RN	SEQUENCE.				
RP	MEDLINE-96332419; PubMed-8769108;				
RA	Itig E.C., Troxler H., Buerigisser D.M., Kuster T., Markert M.,				
RA	Guignard F., Hanzlker P., Birchler N., Heizmann C.W.;				
RT	"Amino acid sequence determination of human S100A12 (p6, calgranulin C, CGRP, CAAF1) by tandem mass spectrometry."				
RT	Biochem. Biophys. Res. Commun. 225:146-150(1996).				
RL	[5]				
RN	SEQUENCE OF 1-20.				
RP	MEDLINE-95351965; PubMed-7626002;				
RA	Guignard F., Maue J., Markert M.;				
RT	"Identification and characterization of a novel human neutrophil protein related to the S100 family."				
RT	Biochem. J. 309:395-401(1995).				
RL	[6]				
RN	SUBUNIT: MONOMER.				
CC	-1- TISSUE SPECIFICITY: MONOCYTES AND LYMPHOCYTES.				
CC	-1- MASS SPECTROMETRY: MW=10444; METHOD=ELCTROSPRAY.				

34	147.5	31.5	90	1	S106_HUMAN	P06703 homo sapien
35	147.5	31.5	97	1	S102_BOVIN	P10462 bos taurus
36	146	31.2	110	1	S105_HUMAN	P33763 homo sapien
37	142.5	30.4	89	1	S106_MOUSE	P14069 mus musculu
38	142.5	30.4	90	1	S106_RABIT	P30801 oryctolagus
39	139.5	29.8	90	1	S106_RAT	P05964 rattus norv
40	139.5	29.8	92	1	S106_CHICK	O98953 gallus gall
41	139	29.6	99	1	S11I_PIG	P31950 sus scrofa
42	138.5	29.6	101	1	S107_BOVIN	O28050 bos taurus
43	137.5	29.4	98	1	S113_HUMAN	O99584 homo sapien
44	136	29.1	93	1	S105_MOUSE	O88945 mus musculu
45	131.5	28.1	102	1	S11X_HUMAN	O60417 homo sapien

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISTAR;
 RA Konrad L., Gadius H.J., Annweiler G.;
 RT "Sequence and expression study of calyculin in the rat testis."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ132717; CAB42002.1;
 DR HSSP: P30801; 1A03.
 DR INTERPRO: IPR001751;
 DR INTERPRO: IPR002048;
 DR PFAM: PF00036; ehand: 1.
 DR PFAM: PF01023; S_100; 1.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_1;
 DR PROSITE: PS00303; S100_CABP; 1.
 DR Cyclic.
 KW
 SQ SEQUENCE 89 AA; 10035 MW; 2AA1A4163D57DC87 CRC64;

Query Match 29.8%; Score 139.5; DB 11; Length 89;
 Best Local Similarity 43.8%; Pred. No. 6.4e-06;
 Matches 35; Conservative 18; Mismatches 24; Indels 3; Gaps 2;
 OY 4 LEEHLEGIYNIHQYSVKRGHPDTLSKGLKOLLTKELANTINIKDKAVIDEIFOGD 63
 DB 5 LDOAIGLVAIFHKYSKGKDKHTTSKKELEKIQEL--TIGAKLQDAIARLMDLDR 62
 OY 64 NODQYDFOEFIS-LVAIAL 82
 DB 63 NKQDEVNFOEYVAFGLAL 82

RESULT 12
 ID P79342 PRELIMINARY; PRT: 98 AA.
 AC P79342;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE 8 KDA AMLEXANOX-BINDING PROTEIN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 KYama Y., Shishibori T., Matsutomo M., Yamashita K., Maeta H.,
 Kobayashi R.;
 RT "Molecular cloning of a new 8Kda protein, isolated with Amlexanox
 RT couple d column chromatography."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB001567; BAA19411.1;
 DR HSSP: P08206; 1A4P.
 DR INTERPRO: IPR001751;
 DR INTERPRO: IPR002048;
 DR PFAM: PF01023; S_100; 1.
 SQ SEQUENCE 98 AA; 11233 MW; 77858426025E643B CRC64;

Query Match 26.4%; Score 123.5; DB 6; Length 98;
 Best Local Similarity 33.3%; Pred. No. 0.00021;
 Matches 26; Conservative 20; Mismatches 29; Indels 3; Gaps 1;
 OY 1 MTKLEHLEGIYNIHQYSVKRGHPDTLSKGLKOLLTKELANTINIKDKAVIDEIFOG 60
 DB 6 LTELKALITVYTTFTFGREGRKSKLSVNEKELVQLPL--LADVSLDEKMS 62
 OY 61 LDANODEYDFOEFISLV 78
 DB 63 FVNDQSEIKFSEYVRLI 80

RESULT 13
 ID Q9UDP3 PRELIMINARY; PRT: 104 AA.
 AC Q9UDP3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE WUSC: LNH0456N16.1 PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99063792; PubMed-9847074;
 RA Sulston J.E., Waterston R.;
 RT "Toward a complete human genome sequence."
 RL Genome Res. 8:1097-1108(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA All J., Wohlmann P., Duckels G.;
 RT "The sequence of Homo sapiens BAC clone RP11-456N16."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.H.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006379; AAD21786.1;
 DR HSSP: P08206; 1A4P.
 DR INTERPRO: IPR001751;
 DR INTERPRO: IPR002048;
 DR PFAM: PF01023; S_100; 1.
 SQ SEQUENCE 104 AA; 11509 MW; 2316AEC84C9CF12A CRC64;

Query Match 25.7%; Score 120.5; DB 4; Length 104;
 Best Local Similarity 32.9%; Pred. No. 0.00042;
 Matches 26; Conservative 19; Mismatches 33; Indels 1; Gaps 1;
 OY 8 LGGIYNIHQYSVKRGHPDTLSKGLKOLLTKELANTINIKDKAVIDEIFOGDANODE 67
 DB 14 IQLAVFQKYGKDGKGNCLSTFELSFMTLELAFTNOKDPGLDRM-KLDVSSDG 72
 OY 68 QYDFOEFISLVAIALKAH 86
 DB 73 QIDFFKFLNLIGGLAVACH 91

RESULT 14
 ID Q9OVR5 PRELIMINARY; PRT: 83 AA.
 AC Q9OVR5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE CALPROTECTIN LARGER COMPONENT MRP-14 (FRAGMENT).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95395365; PubMed-7665986;
 RA Yui S., Mikami M., Yamazaki M.;
 RT "Purification and characterization of the cytotoxic factor in rat
 RT peritoneal exudate cells: its identification as the calcium binding
 RT protein complex, calprotectin."
 RL J. Leukoc. Biol. 58:307-316(1995).

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ID 09TV56 PRELIMINARY: PRT: 101 AA.
AC 09TV56;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE METASTASIN.
GN MTS1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADIN-DARBY; TISSUE-MADIN DARBY CANINE KIDNEY (MDCK);
RA Miyamori H., Hasegawa K., Kim K., Sato H.;
RT "Expression of metastasis associated mts1 gene is co-induced with
RT membrane type-1 matrix metalloproteinase (MT1-MMP) during oncogenic
RT transformation and tubular formation of madin darby canine kidney
RT (MDCK) epithelial cells."
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
L EMBL: AB031064; BAA83419.1; -
DR HSSP: P0801; 1A03;
DR INTERPRO: IPR001751; -
DR INTERPRO: IPR002048; -
DR PFAM: PF00036; ehand; 1.
DR PFAM: PF01023; S.100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE: PS00303; S100_CBP; 1.
SQ SEQUENCE 101 AA; 11847 MW; 5535387DB7577DF0 CRC64;

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Query Match 31.9%; Score 149.5; DB 6; Length 101;
Best Local Similarity 40.0%; Pred. No. 9.1e-07;
Matches 32; Conservative 21; Mismatches 24; Indels 3; Gaps 1;

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QY 4 LEFHLEGIYNIHQYSVKRGHEDTLKSKELQLTRELANTIKNKDAVIDEITFOGLDA 63
DB 5 LEKALDVMTYFHKYSGKEDKFLNRSLEKELMELPSFLGKRTDEAFAOKLMSNIDS 64
QY 64 NDEQVDPQD---FISLVAI 80
DB 65 NRDNEVDFQECVFLSCVAM 84

RESULT 9
QYH57 PRELIMINARY: PRT: 217 AA.
AC 09YH57;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE P26OLF.
GN P26OLF CDNA.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OLFACTORY;
RA MEDLINE-99008915; PubMed-9791000;
RA Miwa N., Kobayashi M., Takamatsu K., Kawamura S.;
RT "Purification and molecular cloning of a novel calcium-binding
RT protein, p26OLF, in the frog olfactory epithelium."
RT Blochem. Biophys. Res. Commun. 251:860-867(1998).
RL EMBL: D50333; BAA34588.1; -
DR HSSP: P08206; 1A4P.
DR INTERPRO: IPR001751; -
DR INTERPRO: IPR002048; -
DR PFAM: PF01023; S.100; 2.
SQ SEQUENCE 217 AA; 24494 MW; 0403689A9E43810B CRC64;

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Query Match 30.9%; Score 144.5; DB 13; Length 217;
Best Local Similarity 32.2%; Pred. No. 6.2e-06;
Matches 29; Conservative 28; Mismatches 28; Indels 5; Gaps 2;

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QY 2 TKLEEHLEGIYNIHQYSVKRGHEDTLKSKELQLTRELANTIKNKD-KAYIDEITFO- 59
DB 10 TEMERSMEKTIYFQYRAGKEGNTSNMFEQDFNVAELGSPKNOQDPAILRKIMKS 69
QY 60 ---GLDANODEQVDFQEFISLVAIALKAH 86
DB 70 VDGSGVDGKQDGEIDFQEFNLIGGMVACH 99

RESULT 10
QYH57 PRELIMINARY: PRT: 495 AA.
AC 09UBG3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE TUMOR RELATED PROTEIN.
GN DRCL OR PDRC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu Z.X., Wang M.R., Cai Y., Xu X., Han Y.L., Wang X.Q., Wu M.;
RT "Cloning and characterization of a novel gene associated with human
RT cancer."
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
L [2]
RC SEQUENCE FROM N.A.
RA Xu Z.X., Wang M.R., Cai Y., Xu X., Han Y.L., Wang X.Q., Wu M.;
RT "Cloning and characterization of a novel cDNA associated with human
RT cancer."
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
L EMBL: AF185276; AAF00514.1; -
DR EMBL: AF077831; AAD55747.1; -
DR HSSP: P02633; SICB.
DR INTERPRO: IPR001751; -
DR INTERPRO: IPR002048; -
DR PFAM: PF00036; ehand; 1.
DR PFAM: PF01023; S.100; 1.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 495 AA; 53533 MW; CA882A11B4E64DC3 CRC64;

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```

Query Match 30.8%; Score 144; DB 4; Length 495;
Best Local Similarity 37.2%; Pred. No. 1.7e-05;
Matches 29; Conservative 21; Mismatches 28; Indels 0; Gaps 0;

```

```

QY 1 MKLEEHLEGIYNIHQYSVKRGHEDTLKSKELQLTRELANTIKNKDAVIDEITFOG 60
DB 1 MPOLLQNTIGTIEAFRRARREGCTALTRELKRLLEQERADVIYKPHDPAIDVETLRL 60
QY 61 LDANODEQVDFQEFISLV 78
DB 61 LDEHDTGTVEKFEFLV 78

RESULT 11
QYH2B7 PRELIMINARY: PRT: 89 AA.
AC 09R2B7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE CALCYCLIN.
GN CACY.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

RT domain at the amino terminus";
 RL Biol. Chem. 267:23772-23781(1992).
 CC -1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
 CC DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
 CC TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
 CC -1- PTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
 CC HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
 CC 324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.
 CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
 CC PROTEOLYTICALLY CLEAVED.
 CC -1- POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOUND
 CC WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
 CC REPEATS.
 CC EMBL: L01089; AAA60177.1; -;
 CC EMBL: L01090; AAA60176.1; -;
 CC HSSP: P02638; ICFP.
 CC MIM: J35940; -;
 CC INTERPRO: IPR001751; -;
 CC INTERPRO: IPR002048; -;
 CC PFAM: PF00036; etfhand; 1.
 CC PFAM: PF01023; S_100; 1.
 CC PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 CC PROSITE: PS00303; S100_CABP; 1.
 CC POLYMORPHISM.
 CC PROPER 1 293 POTENTIAL.
 CC CHAIN 294 467 FILAGGRIN.
 CC PROPER 468 474 POTENTIAL.
 CC CHAIN 475 >591 FILAGGRIN.
 CC SITE 1 (BY SIMILARITY).
 CC SITE 2 (BY SIMILARITY).
 CC SITE II (BY SIMILARITY).
 CC NON_TER 591 591
 CC SEQUENCE 591 AA; 66366 MW; 381491625C75E369 CRC64;

Query Match 35.9%; Score 168; DB 4; Length 591;
 Best Local Similarity 39.1%; Pred. No. 1.4e-07;
 Matches 36; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKOLLTKELANTINKKAKAVIDEFG 60
 DB 1 MSTLLEVFALINLFNKYSKDKNTDLSKKELEKEFEOLKNPDDPDVMDH 60
 OY 61 LDANODEVDQFDFISLVAIALAKAAHYTHKE 92
 DB 61 LDIDHNKKIDFTEFLMVFRLAQAYESTRKE 92
 RESULT 6
 331
 AC 005331 PRELIMINARY; PRT; 1218 AA.
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE FILAGGRIN (PROFILAGGRIN) (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FORESKIN;
 RX MEDLINE=93109348; PubMed=8417356;
 RA Markov N.G., Marekov L.N., Chipcev C.C., Gan S.-O., Idler W.W.,
 RA Stelhaert P.M.;
 RL "Profilaggrin is a major epidermal calcium-binding protein.";
 RL Mol. Cell. Biol. 13:613-625(1993).
 CC -1- FUNCTION: AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES
 CC DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING
 CC TERMINAL DIFFERENTIATION OF MAMMALIAN EPIDERMIS.
 CC -1- PTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS A LARGE, INSOLUBLE,
 CC HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF
 CC 324 AA. THE PRECURSOR IS DEPOSITED AS KERATOHYALIN GRANULES.

CC DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &
 CC PROTEOLYTICALLY CLEAVED.
 CC -1- POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOUND
 CC WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
 CC REPEATS.
 CC EMBL: M96943; AAA36487.1; -;
 CC HSSP: P02638; ICFP.
 CC INTERPRO: IPR001751; -;
 CC INTERPRO: IPR002048; -;
 CC PFAM: PF00036; etfhand; 1.
 CC PFAM: PF01023; S_100; 1.
 CC PROSITE: PS00018; EF_HAND; UNKNOWN_1.
 CC PROSITE: PS00303; S100_CABP; 1.
 CC Phosphorylation; Polyprotein; Developmental protein; Calcium-binding;
 CC POLYMORPHISM.
 CC SITE I (BY SIMILARITY).
 CC SITE II (BY SIMILARITY).
 CC NON_TER 1218 1218
 CC SEQUENCE 1218 AA; 133604 MW; EC195AD5285B19C2 CRC64;

Query Match 33.8%; Score 158; DB 4; Length 1218;
 Best Local Similarity 37.0%; Pred. No. 2.5e-06;
 Matches 34; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

OY 1 MTKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKOLLTKELANTINKKAKAVIDEFG 60
 DB 1 MSTLLEVFALINLFNKYSKDKNTDLSKKELEKEFEOLKNPDDPDVMDH 60
 OY 61 LDANODEVDQFDFISLVAIALAKAAHYTHKE 92
 DB 61 LDIDHNKKIDFTEFLMVFRLAQAYESTRKE 92

RESULT 7
 09JUL08
 ID 09JUL08 PRELIMINARY; PRT; 79 AA.
 AC 09JUL08
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE S100 CALCIUM BINDING PROTEIN A1 (FRAGMENT).
 GN S100A1.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Klevitz R., Lyons G.E., Schafer B.W., Helzmann C.W.;
 RA "Transcriptional regulation of S100A1 and expression during mouse
 RA heart development.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF218353; AAF32320.1; -;
 FT NON_TER 79 79
 CC SEQUENCE 79 AA; 8863 MW; F94EDA3A798815D5 CRC64;

Query Match 32.9%; Score 154; DB 11; Length 79;
 Best Local Similarity 40.3%; Pred. No. 2.7e-07;
 Matches 31; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

OY 2 TKLEHLEGIIVNIFHOYSVRKGFDTLSKGLKOLLTKELANTINKKAKAVIDEFG 61
 DB 3 SELESAMETLINVFHSAQSGDKYLSKKELEKDLLOTELSGLDVOKDADAVKMKEL 62
 OY 62 DANODEVDQFDFISLV 78
 DB 63 DENGDEVDPEKVVAV 79

RESULT 8
 09TV56

AC 09NW0;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14 VARIANT E.
 GN S100A9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.,
 RT "Human gene for migration inhibitory factor-related protein 14
 (MRP14), variant allele."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF37582; AAF62537.1;
 SQ SEQUENCE 114 AA; 13261 MW; D701528635F4DBC2 CRC64;

any Match 44.1%; Score 206.5; DB 4; Length 114;
 -est Local Similarity 45.7%; Pred. No. 6.5e-12;
 Matches 42; Conservative 22; Mismatches 27; Indels 1; Gaps 1;

QY 1 MTKLEHLEGIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNDKAVIDEIFQ 59
 Db 5 MSQLEHLEGIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNDKAVIDEIFQ 64
 QY 60 GLDANODEQVDFEFTSLVAIALKAHYHTRK 91
 Db 65 DLDTNADKOLFEEFIMLMARLTWASHKME 96

RESULT 3
 ID 093395 PRELIMINARY; PRT; 101 AA.
 AC 093395;
 DT 01-NOV-1998 (Tremblrel. 08, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE S100-LIKE CALCIUM BINDING PROTEIN.
 GN S100.
 OS Salvelinus fontinalis (Brook trout).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobe J.M., Goetz F.M.;
 RT "Downregulation of a S100-like calcium binding protein in the brook
 trout ovary following ovulation."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVULATORY OVARY;
 RA Langenau D.M., Goetz F.M.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF07613; AAC28367.1;
 DR HSSP; P02633; S1CB.
 DR INTERPRO; IPR001751;
 DR INTERPRO; IPR002048;
 DR PRAM; PF00036; ehand; 1.
 DR PRAM; PF01023; S_100; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00303; S100_CABP; 1.
 SQ SEQUENCE 101 AA; 11285 MW; BF45582FF9279DOA CRC64;

Query Match 40.4%; Score 189; DB 13; Length 101;
 Best Local Similarity 43.2%; Pred. No. 2.2e-10;
 Matches 41; Conservative 20; Mismatches 28; Indels 6; Gaps 2;

QY 2 TKLEHLEGIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNDKAVIDEIFQ 61
 Db 3 SQLESMESLITVFHRYADGDCNLTLSKGLKOLLTKELANTIKNDKAVIDEIFQ 62
 QY 62 DANODEQVDFEFTSLVAIALKAHYHTRK 91
 Db 63 DONGDKVSPFEFVSIV-VGLSLACQIYOLHTRK 96

RESULT 4
 ID 09PSF6 PRELIMINARY; PRT; 92 AA.
 AC 09PSF6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE ICTALALCIN.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Siluriformes; Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-94376615; PubMed-8090068;
 RA Bettini E., Porta A.R., Dahmen N., Wang H., Margolis F.L.;
 RT "Expressed sequence tags (EST) identify genes preferentially expressed
 in catfish chemosensory tissues."
 RL Brain Res. Mol. Brain Res. 23:285-291(1994).
 DR HSSP; P30801; IA03.
 DR INTERPRO; IPR001751;
 DR INTERPRO; IPR002048;
 DR PRAM; PF00036; ehand; 1.
 DR PRAM; PF01023; S_100; 1.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 DR PROSITE; PS00303; S100_CABP; 1.
 SQ SEQUENCE 92 AA; 10022 MW; E04875D0C9921C50 CRC64;

Query Match 39.7%; Score 186; DB 13; Length 92;
 Best Local Similarity 46.8%; Pred. No. 3.8e-10;
 Matches 37; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTKLEHLEGIVNIFHOYSVRKGFHPTLSKGLKOLLTKELANTIKNDKAVIDEIFQ 60
 Db 1 MSDLGKMLLITFPHKYSSEBCKTLTKGLKOLLTKELANTIKNDKAVIDEIFQ 60
 QY 61 LDANODEQVDFEFTSLVA 79
 Db 61 LDTNADGVDFEFTATWVA 79

RESULT 5
 ID 001720 PRELIMINARY; PRT; 591 AA.
 AC 001720;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE FLAAGRIN PRECURSOR (PROFLAAGRIN) (FRAGMENT).
 GN FLG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA MEDLINE-93054736; PubMed-1429717;
 RA Presland R.B., Haydock P.V., Fleckman P., Nirunskafiri W., Dale B.A.;
 RT "Characterization of the human epidermal profilaggrin gene. Genomic
 organization and identification of an S-100-like calcium binding

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: June 8, 2001, 15:03:05 ; Search time 19.35 Seconds
(Without alignments)
557.268 Million cell updates/sec

Title: US-09-227-854-2
Perfect score: 468
Sequence: 1 MTKLEHLEGIVNIFHOYSV.....EFISLVAIALKAHHTHKE 92

Scoring table:
BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues
1 number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SP archaea:*
 - 2: SP bacteria:*
 - 3: SP fungi:*
 - 4: SP human:*
 - 5: SP invertebrate:*
 - 6: SP mammal:*
 - 7: SP mhc:*
 - 8: SP organelle:*
 - 9: SP phage:*
 - 10: SP plant:*
 - 11: SP rodent:*
 - 12: SP unclassified:*
 - 13: SP vertebrate:*
 - 14: SP virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	53.0	70	6 Q9TR16	Q9TR16 bos taurus
2	206.5	44.1	114	4 Q9NYMO	Q9NYMO homo sapien
3	189	40.4	101	13 Q93395	Q93395 saliculus
4	186	39.7	92	13 Q9SF6	Q9SF6 ictalurus p
5	168	35.9	591	4 Q01720	Q01720 homo sapien
6	158	33.8	1218	4 Q05331	Q05331 homo sapien
7	154	32.9	79	11 Q9JL08	Q9JL08 mus musculu
8	149.5	31.9	101	6 Q9TV56	Q9TV56 canis famli
9	144.5	30.9	217	13 Q9YH57	Q9YH57 rana catesb
10	144	30.8	495	4 Q9UB63	Q9UB63 homo sapien
11	139.5	29.8	89	11 Q9R2B7	Q9R2B7 rattus norv
12	123.5	26.4	98	6 P79342	P79342 bos taurus
13	120.5	25.7	104	4 Q9UDP3	Q9UDP3 homo sapien
14	117.5	25.1	83	11 Q9OVR5	Q9OVR5 rattus sp.
15	112.5	24.0	73	6 Q28714	Q28714 oryctolagus
16	96	20.5	493	5 Q15872	Q15872 paramecium
17	95	20.3	473	10 Q9SE24	Q9SE24 oryza sativ
18	92.5	19.8	55	6 Q9TSB1	Q9TSB1 bos taurus
19	90	19.2	523	10 Q9SE25	Q9SE25 oryza sativ

20	89.5	19.1	535	10 Q38873	Q38873 arabidopsis
21	89	19.0	564	10 Q9ZTU9	Q9ZTU9 solanum tub
22	88.5	18.9	170	5 Q9NKW7	Q9NKW7 perlinope
23	87.5	18.7	226	10 Q81446	Q81446 arabidopsis
24	87.5	18.7	244	5 Q20804	Q20804 caenorhabdi
25	85.5	18.3	162	5 Q9V315	Q9V315 drosophila
26	84.5	18.1	70	4 Q95663	Q95663 homo sapien
27	84.5	18.1	146	10 Q23480	Q23480 arabidopsis
28	84.5	18.1	167	4 Q9NZ08	Q9NZ08 homo sapien
29	84.5	18.1	167	6 Q9N1R1	Q9N1R1 bos taurus
30	84.5	18.1	167	11 Q9JLK6	Q9JLK6 mus musculu
31	84.5	18.1	226	6 Q9N1R0	Q9N1R0 bos taurus
32	84.5	18.1	227	4 Q9NZU7	Q9NZU7 homo sapien
33	84.5	18.1	227	11 Q9JLK7	Q9JLK7 mus musculu
34	83.5	17.8	163	11 Q9JLK5	Q9JLK5 mus musculu
35	83.5	17.8	216	11 Q9JLK4	Q9JLK4 mus musculu
36	83.5	17.8	248	10 Q65587	Q65587 arabidopsis
37	83	17.7	169	5 Q9NEM1	Q9NEM1 schistosoma
38	82.5	17.6	220	4 Q9NPM3	Q9NPM3 homo sapien
39	82.5	17.6	226	10 Q81447	Q81447 arabidopsis
40	82.5	17.6	571	10 Q48827	Q48827 arabidopsis
41	80	17.1	536	10 Q65644	Q65644 arabidopsis
42	79.5	17.0	163	6 Q9N1O9	Q9N1O9 bos taurus
43	79.5	17.0	553	10 Q80700	Q80700 arabidopsis
44	78.5	16.8	298	11 Q88751	Q88751 rattus norv
45	78.5	16.8	309	2 Q51695	Q51695 borrelia bu

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	70 AA.
Q9TR16	Q9TR16			
AC	Q9TR16			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-OCT-2000 (Tremblrel. 15, Last annotation update)			
DE	CORNER-ASSOCIATED ANTIGEN, CO-AG-CALGRANULIN C HOMOLOG.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OX	NCBI_Taxid-9913;			
RN	[1]			
RP	SEQUENCE.			
RA	MEDLINE-96181454; Pubmed-8603881;			
RA	Liu S.H., Gottsch J.D.;			
RT	"Amino acid sequence of an immunogenic corneal stromal proteo.."			
RL	Invest. Ophthalmol. Vis. Sci. 37:944-948(1996).			
DR	HSP; P02638; IMHO.			
DR	INTERPRO: IPR001751;			
DR	INTERPRO: IPR002048;			
DR	PFAM: PF01023; S.100; 1.			
SO	SEQUENCE 70 AA; 8134 MW; 7D52BEA97A4D53A5 CRC64;			

Query Match	53.0%; Score 248; DB 6; Length 70;
Best Local Similarity	68.6%; Pred. No. 6.1e-16;
Matches	48; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY	2 TKELEHLEGIVNIFHOYSVRKGHDTLSKGLTKLLKELANTIKNKDRAVIDEIOGL 61
DB	1 TKLEHLEGIVNIFHOYSVRKGHDTLNKRELKLTREKLTONTKDDPTDIKIRODL 60
QY	62 DANODEQVDF 71
DB	61 DADKKAVVF 70
RESULT	2
Q9NYMO	PRELIMINARY;
Q9NYMO	PRT; 114 AA.